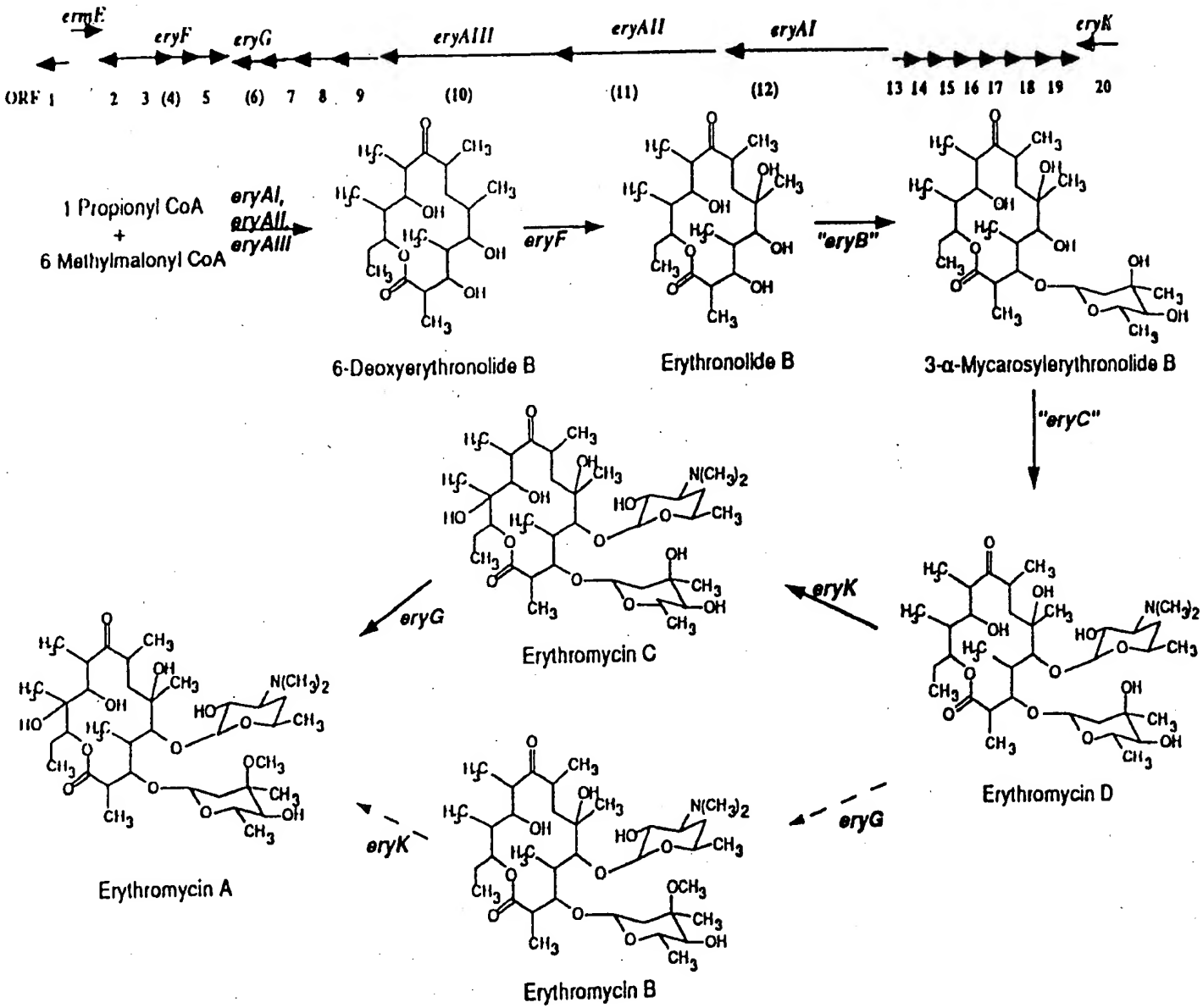


Figure 1

Figure 2

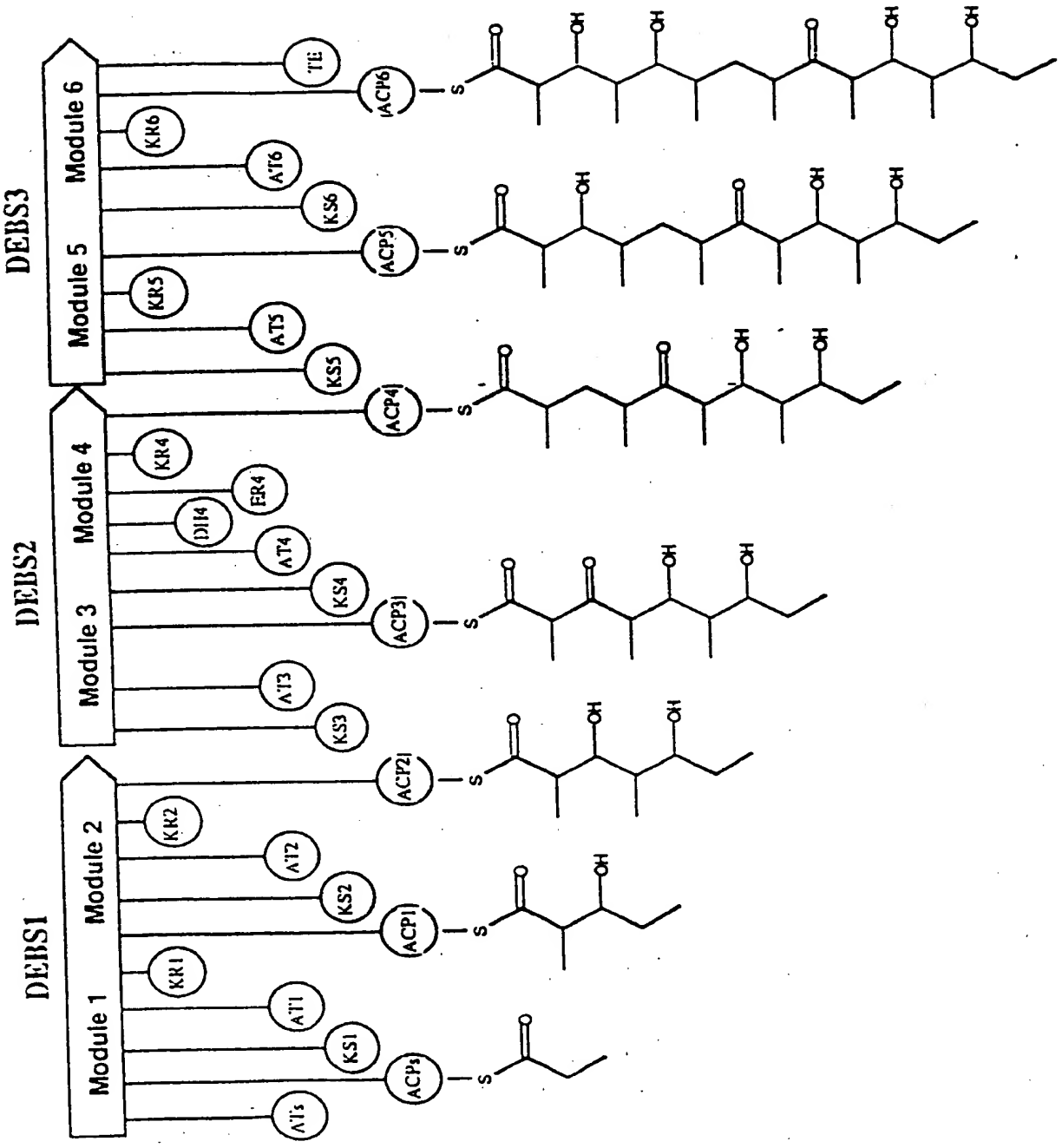

DEBS1
Module 1
Module 2
DEBS2
Module 3
Module 4
DEBS3
Module 5
Module 6
AT's
KS1
AT1
KR1
ACP1
KS2
AT2
KR2
ACP2
KS3
AT3
ACP3
KS4
AT4
DH4
ER4
KR4
ACP4
KS5
AT5
KR5
ACP5
KS6
AT6
KR6
ACP6
TE
S

Figure 3

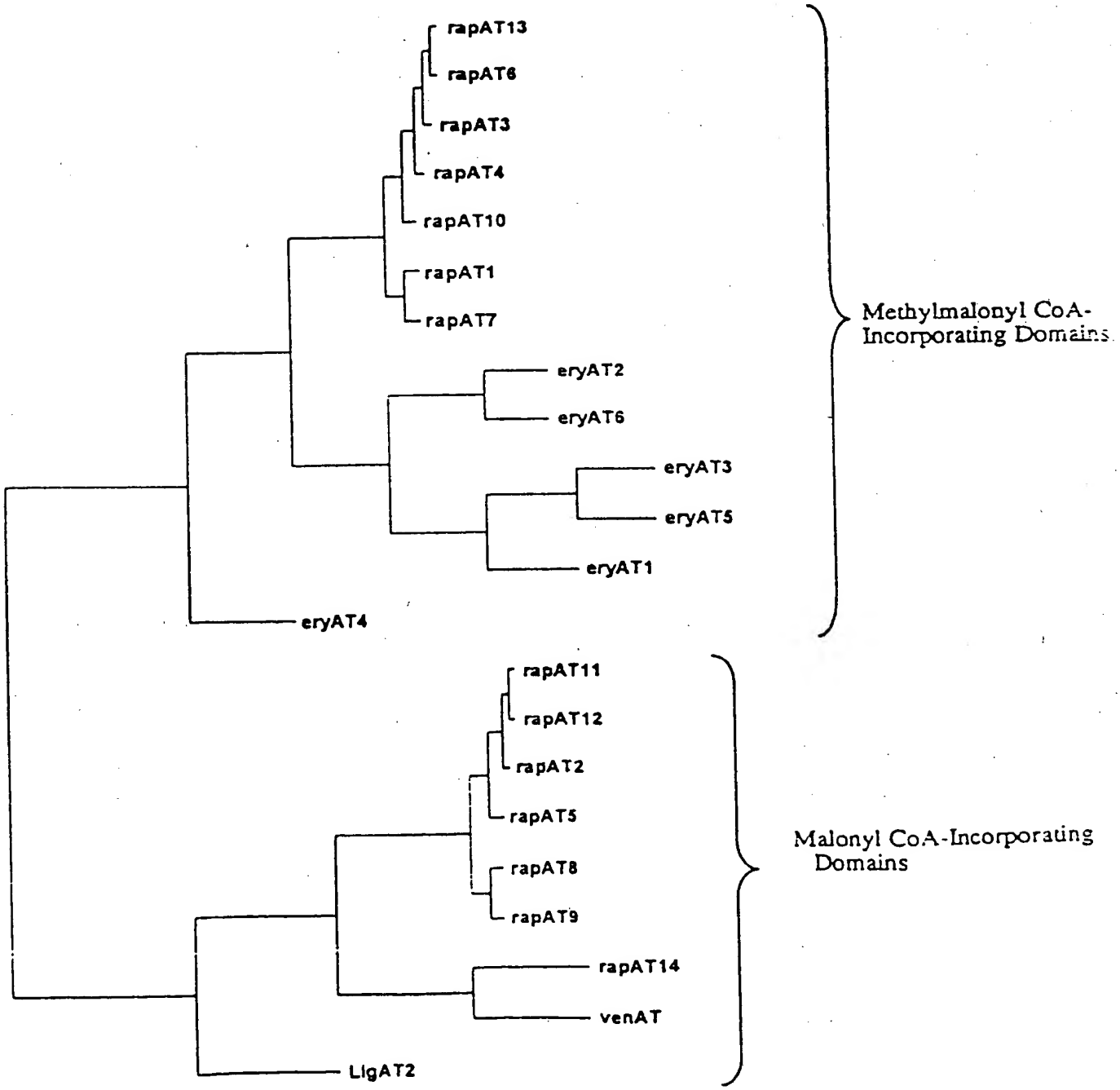

rapAT13
rapAT6
rapAT3
rapAT4
rapAT10
rapAT1
rapAT7
eryAT2
eryAT6
eryAT3
eryAT5
eryAT1
eryAT4
rapAT11
rapAT12
rapAT2
rapAT5
rapAT8
rapAT9
rapAT14
venAT
LlgAT2
Methylmalonyl CoA-Incorporating Domains
Malonyl CoA-Incorporating Domains

Figure 4a

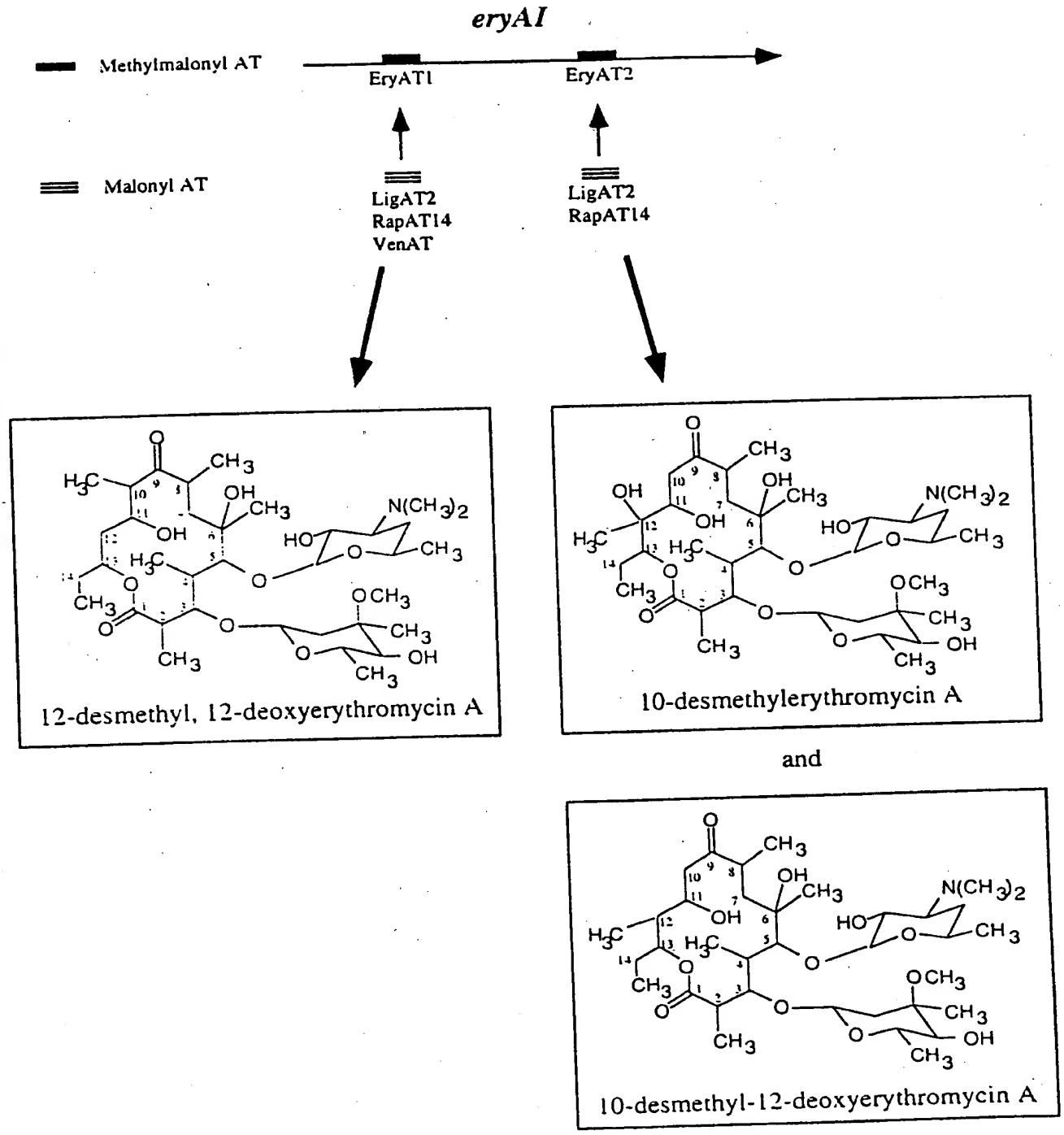
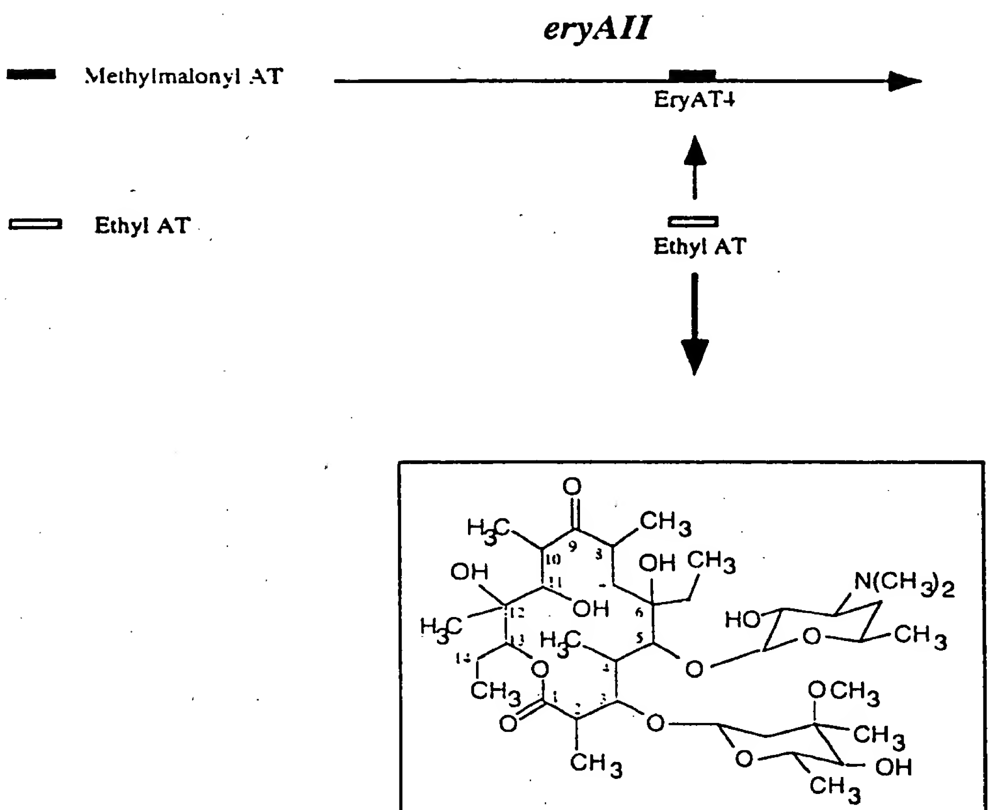
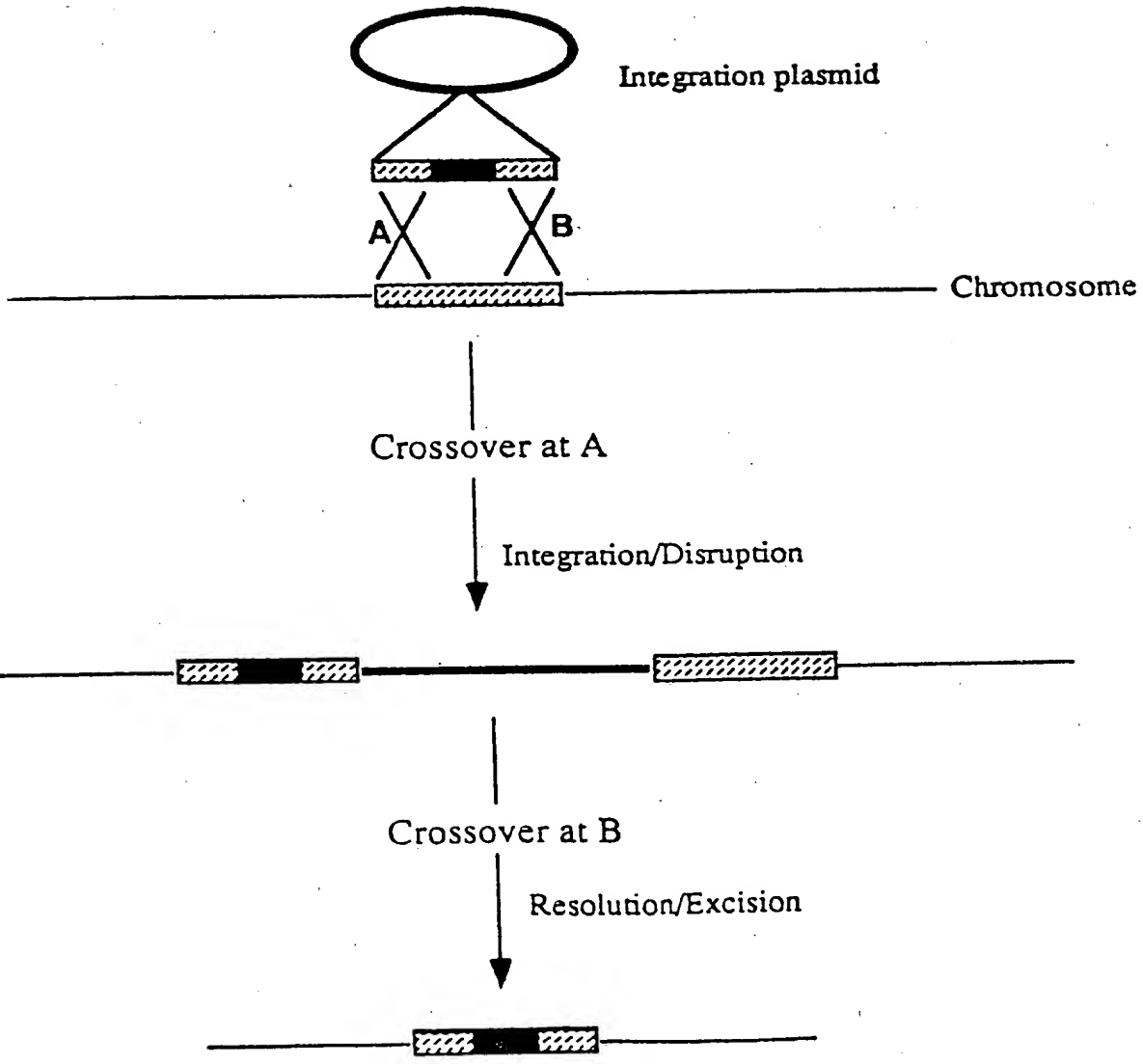

eryAI
Methylmalonyl AT
EryAT1
EryAT2
Malonyl AT
LigAT2
RapAT14
VenAT
LigAT2
RapAT14
12-desmethyl, 12-deoxyerythromycin A
10-desmethylerythromycin A
and
10-desmethyl-12-deoxyerythromycin A

Figure 4b



6-desmethyl-6-ethylerythromycin A

Figure 5


Integration plasmid
A
B
Chromosome
Crossover at A
Integration/Disruption
Crossover at B
Resolution/Excision

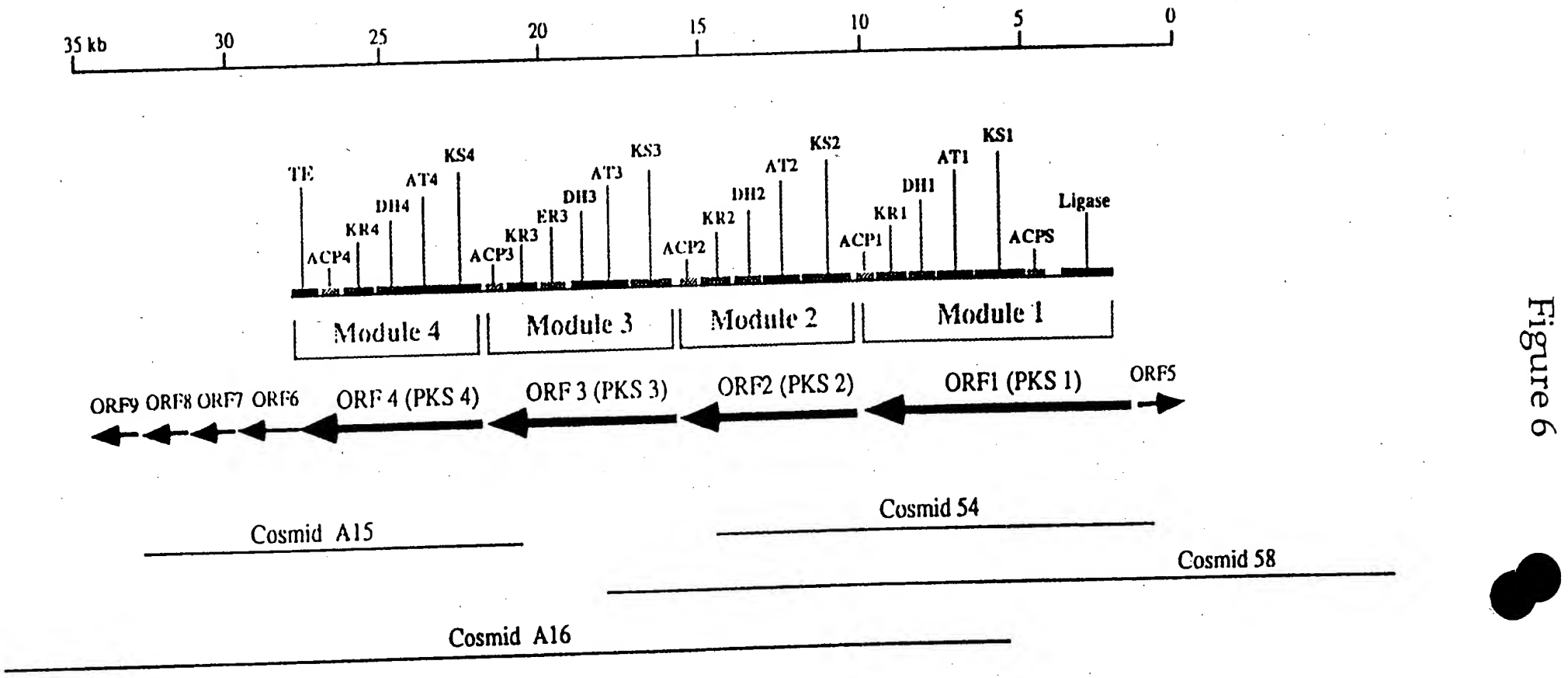


Figure 6

Figure 7

```
GGGCCGCTGGCGGTGATGTTCACCGGACAGGGCTCCCAACGCCCCGGCATGGGACGACAG   60
G  P  L  A  V  M  F  T  G  Q  G  S  Q  R  P  G  M  G  R  Q     20

TTGTACGAGCACTTCCCCGTCTTCGCCCAGGCACTGGACGAGGTCTTCGCACTCGCCACC   120
L  Y  E  H  F  P  V  F  A  Q  A  L  D  E  V  F  A  L  A  T     40

CCCGGACTACGCGAGGTGATGTTCGACCCCGACCAGGCCGAAACACTCCAACGCACCGAC   180
P  G  L  R  E  V  M  F  D  P  D  Q  A  E  T  L  Q  R  T  D     60

CACGCCCAGATCGCCCTGTTCGCCTTCGAAACCGCCCTCTACCGACTCTGGGAATCCTGG   240
H  A  Q  I  A  L  F  A  F  E  T  A  L  Y  R  L  W  E  S  W     80

GGCCTGCGACCCGACATGGTCTGCGGACACTCGGTCGGAGAAATCACCGCAGCCCACGTC   300
G  L  R  P  D  M  V  C  G  H  S  V  G  E  I  T  A  A  H  V     100

TCCGGCACCCTCACCCTCCCCGACGCCGTCCACCTCGTCACCACACGCGGCACCCTCATG   360
S  G  T  L  T  L  P  D  A  V  H  L  V  T  T  R  G  T  L  M     120

CAAAACCTGCCCCCCGGCGGCGCCATGCTCGCCGTCGCCACCGACCCCCACACCCTCCAA   420
Q  N  L  P  P  G  G  A  M  L  A  V  A  T  D  P  H  T  L  Q     140

CCCCACCTCGACAACCACCACGACACCATCTCCATCGCCGCCATCAACGGCCCCCACGCC   480
P  H  L  D  N  H  H  D  T  I  S  I  A  A  I  N  G  P  H  A     160

ACCGTCCTCTCCGGCGACCGCACCACCCTCCACCACATCGCCACCCAACTCAACACCAAA   540
T  V  L  S  G  D  R  T  T  L  H  H  I  A  T  Q  L  N  T  K     180

ACCAACTGGCTCAACGTCAGCCACGCCTTCCACTCCCCCCTCATGCAACCCATCCTCCAA   600
T  N  W  L  N  V  S  H  A  F  H  S  P  L  M  Q  P  I  L  Q     200

CCCTTCACCACCACCCTCAACACCCTCACCCACCACCCCCCACACACACCCCTCATCAGC   660
P  F  T  T  T  L  N  T  L  T  H  H  P  P  H  T  P  L  I  S     220

ATGCTCACCGCCACACCCACCCACCCCGACACCACCCACTGGACCCAGCACATCACCGCA   720
M  L  T  A  T  P  T  H  P  D  T  T  H  W  T  Q  H  I  T  A     240

CCCGTCCGCTACACCGACACCCTCCACCACCTCCACCACCACGGCATCACCACCTACCTC   780
P  V  R  Y  T  D  T  L  H  H  L  H  H  H  G  I  T  T  Y  L     260

GAAATCGGCCCCGACACCACCCTCACCGCCCTCGCCCGCACCACCCTCCCCACCACCACC   840
E  I  G  P  D  T  T  L  T  A  L  A  R  T  T  L  P  T  T  T     280

CACCTCATCCCCACCACCCGCCGCAACCACAACGAAGTCCGCAGCACGAACGAGGCGTTG   900
H  L  I  P  T  T  R  R  N  H  N  E  V  R  S  T  N  E  A  L     300

GGCAGGGTGTTCAGCGTGGGCCACTCGGTGGACTGGCGGGCCCTCACTCCGACCGGGAGG   960
G  R  V  F  S  V  G  H  S  V  D  W  R  A  L  T  P  T  G  R     320

CGTACCTCCCTGCCGACGTACCCCT        935
R  T  S  L  P  T  Y  P     328
```

Figure 8

PCR oligos:

*Avr*II

N-terminal Oligo: 5' *Eco*RI Tag-CCTAGGCTGGCGGTGATGTTCA-3'
GGGCC

Engineered *Avr*II | Homologous region

*Nsi*I

C-terminal Oligo: 5' *Bam*HI Tag-ATGCATACGTCGGCAGGGAGGTAC-3'
G GG

Engineered *Nsi*I | Homologous region

PCR cloning:

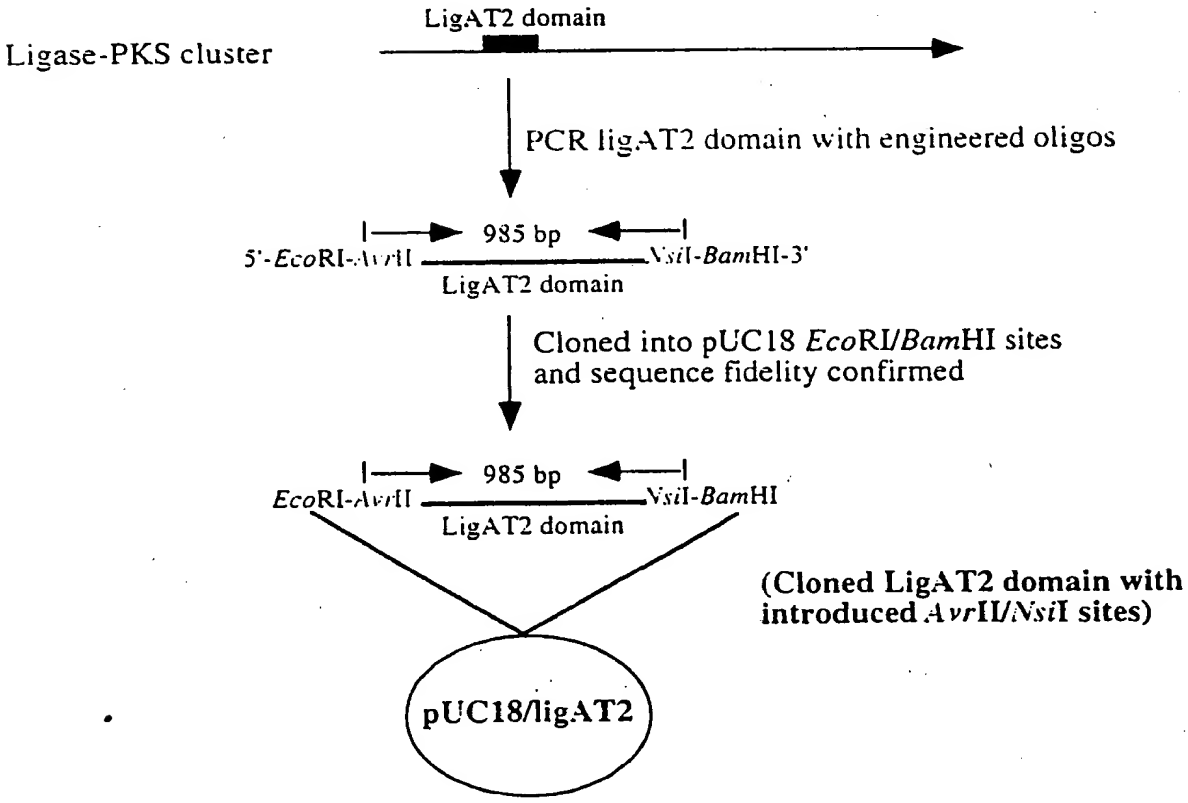


Figure 9

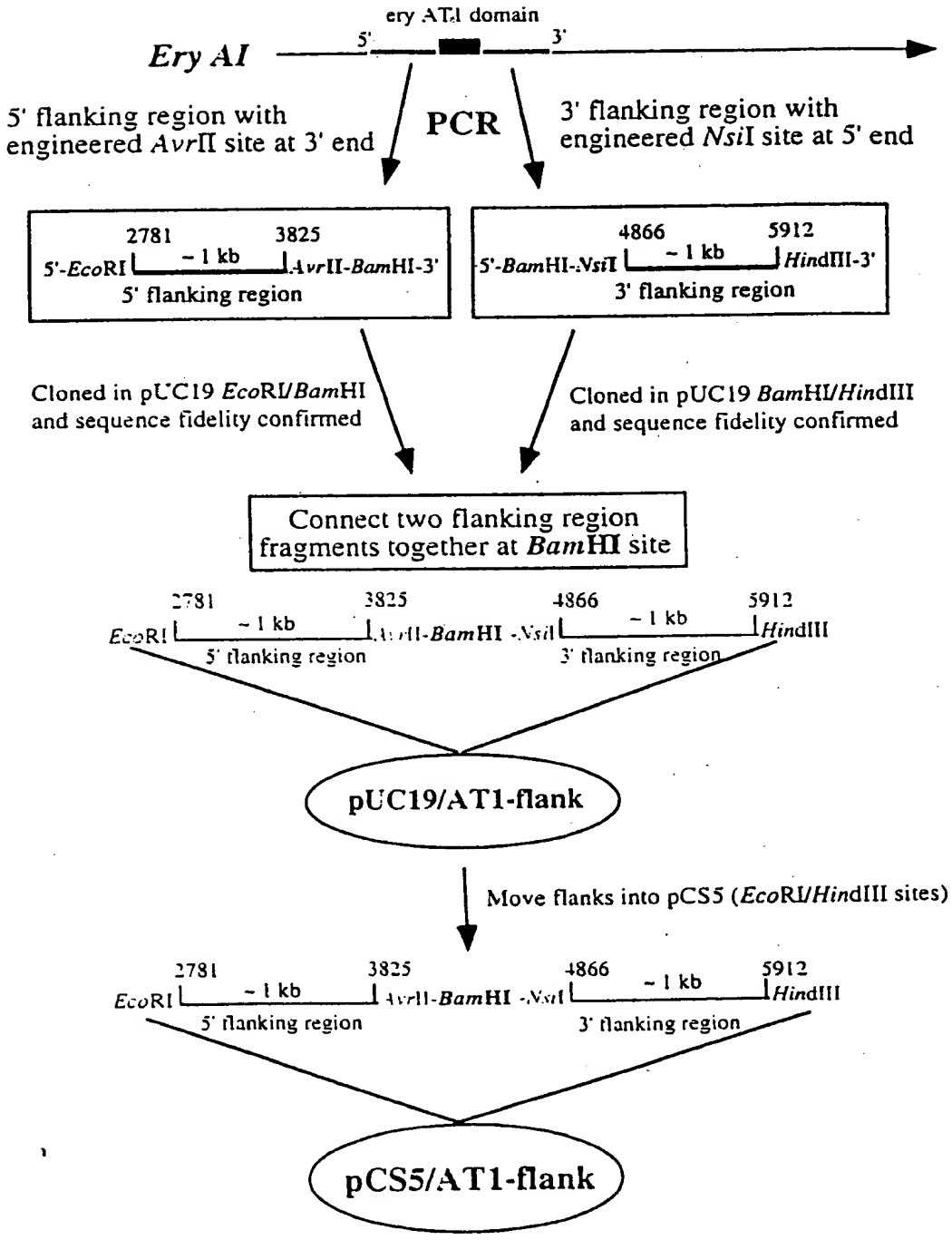

ery AT1 domain
Ery AI
5'
3'
5' flanking region with engineered AvrII site at 3' end
PCR
3' flanking region with engineered NsiI site at 5' end
2781
3825
5'-EcoRI
~ 1 kb
AvrII-BamHI-3'
5' flanking region
4866
5912
5'-BamHI-NsiI
~ 1 kb
HindIII-3'
3' flanking region
Cloned in pUC19 EcoRI/BamHI and sequence fidelity confirmed
Cloned in pUC19 BamHI/HindIII and sequence fidelity confirmed
Connect two flanking region fragments together at BamHI site
2781
3825
4866
5912
EcoRI
~ 1 kb
AvrII-BamHI
NsiI
~ 1 kb
HindIII
5' flanking region
3' flanking region
pUC19/AT1-flank
Move flanks into pCS5 (EcoRI/HindIII sites)
2781
3825
4866
5912
EcoRI
~ 1 kb
AvrII-BamHI
NsiI
~ 1 kb
HindIII
5' flanking region
3' flanking region
pCS5/AT1-flank

Figure 10

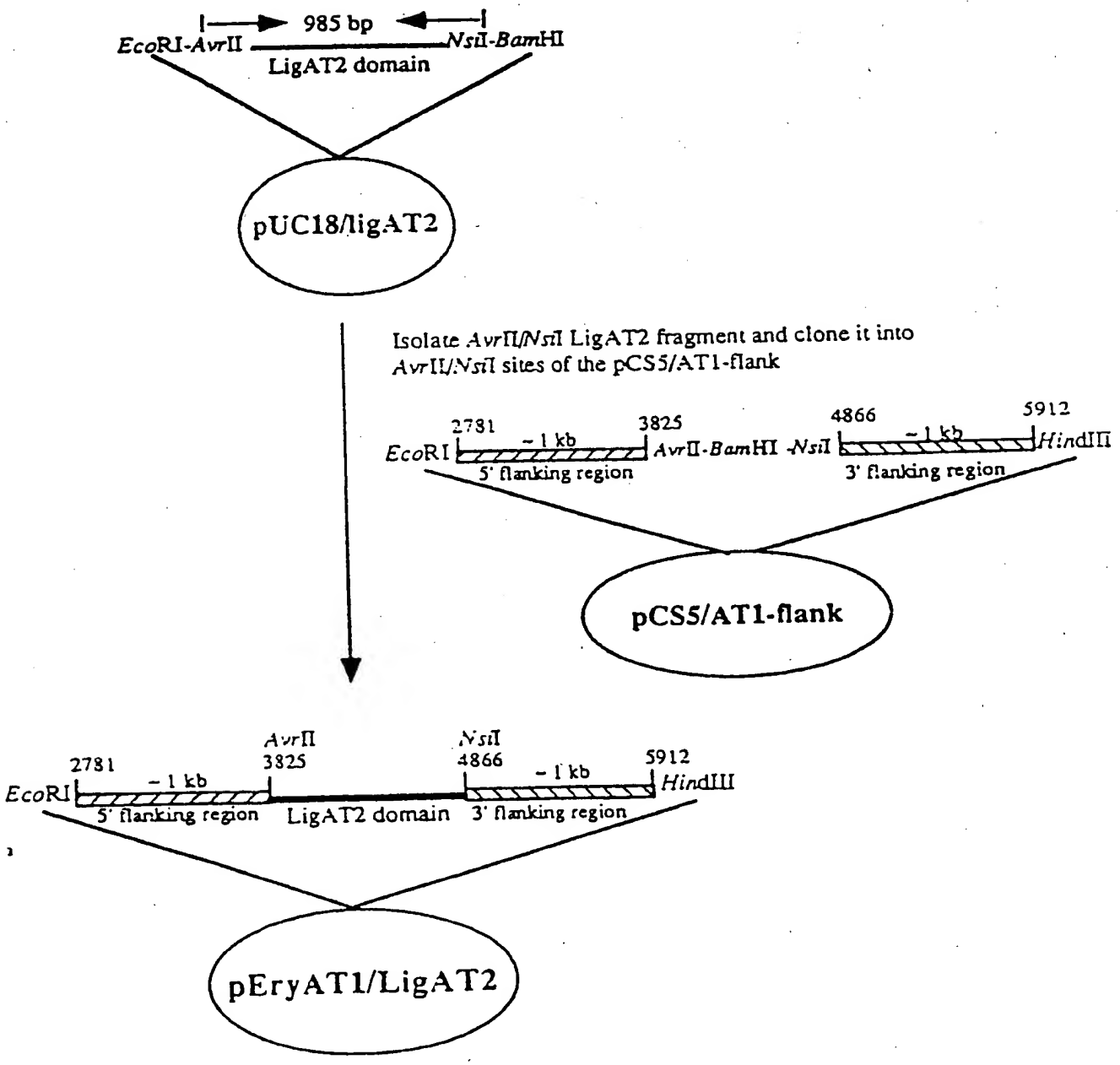

985 bp
EcoRI-AvrII
NsiI-BamHI
LigAT2 domain
pUC18/ligAT2
Isolate AvrII/NsiI LigAT2 fragment and clone it into AvrII/NsiI sites of the pCS5/AT1-flank
2781
~ 1 kb
3825
EcoRI
AvrII-BamHI
4866
NsiI
~ 1 kb
5912
HindIII
5' flanking region
3' flanking region
pCS5/AT1-flank
AvrII
3825
NsiI
4866
2781
~ 1 kb
5912
EcoRI
~ 1 kb
HindIII
5' flanking region
LigAT2 domain
3' flanking region
pEryAT1/LigAT2

Figure 11

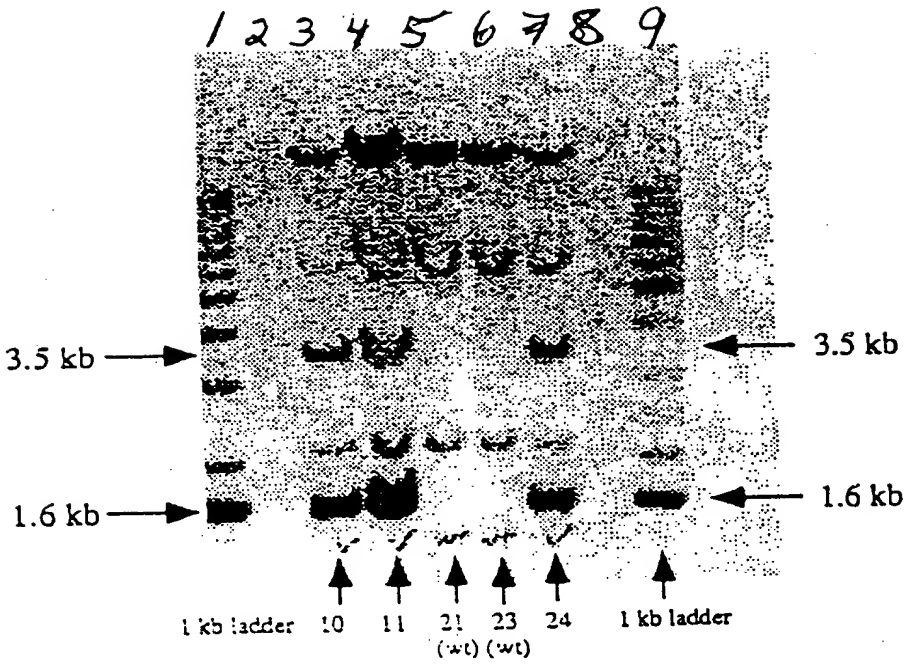


Figure 12

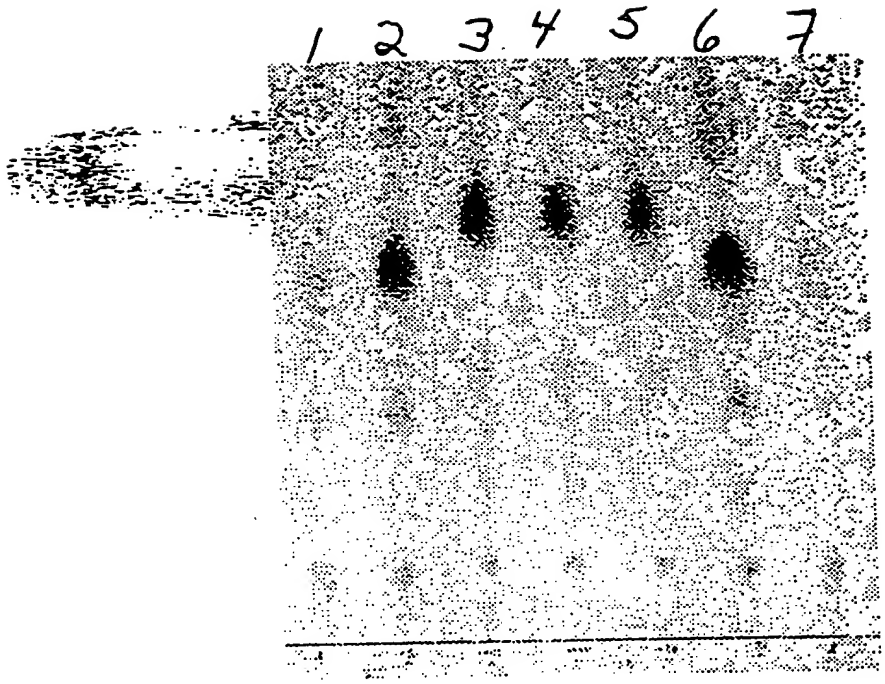


Figure 13

Construction of eryAT2 flanking regions in pCS5

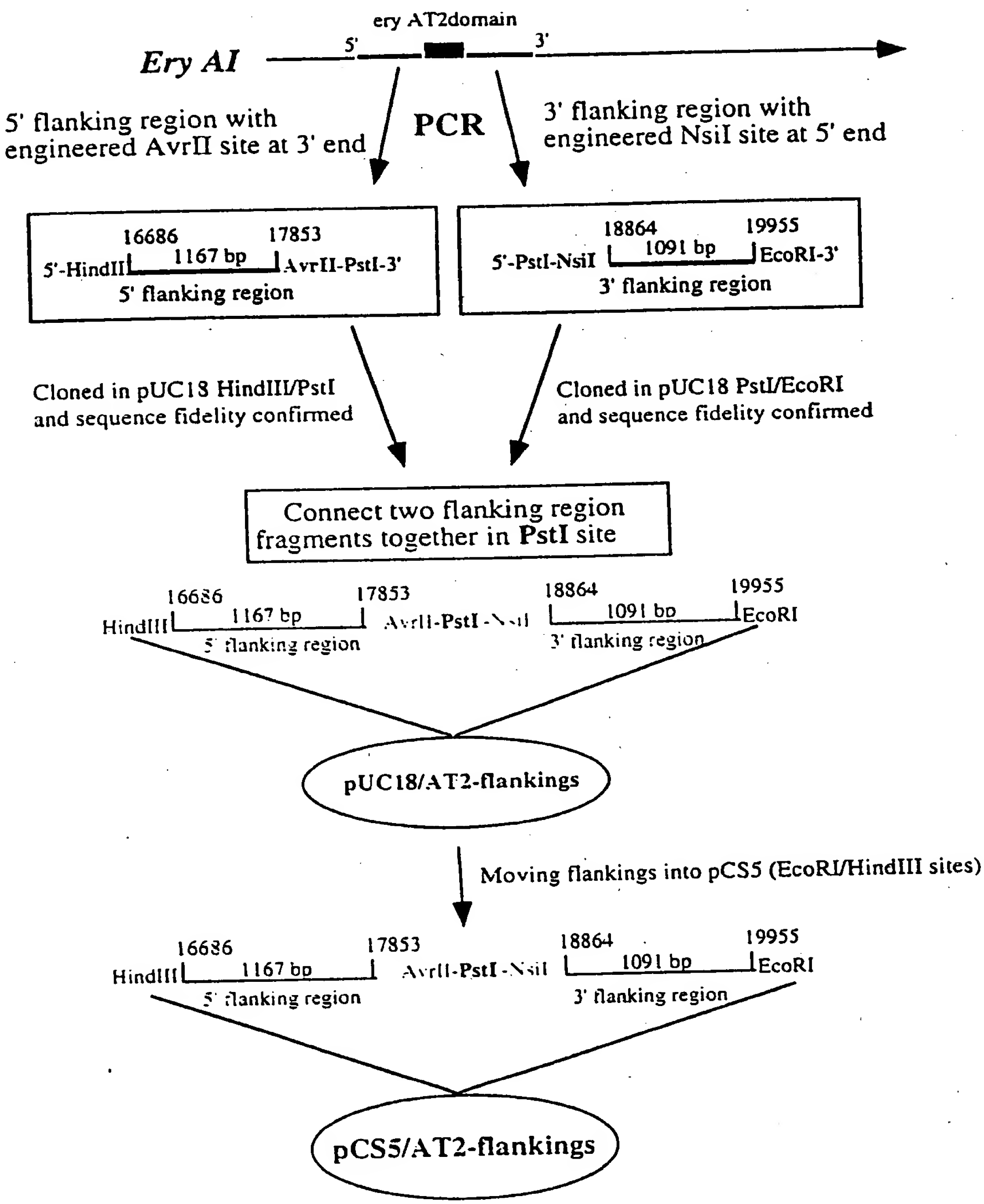


Figure 14

Scheme for Construction of pEryAT2/LigAT2 Integration Plasmid

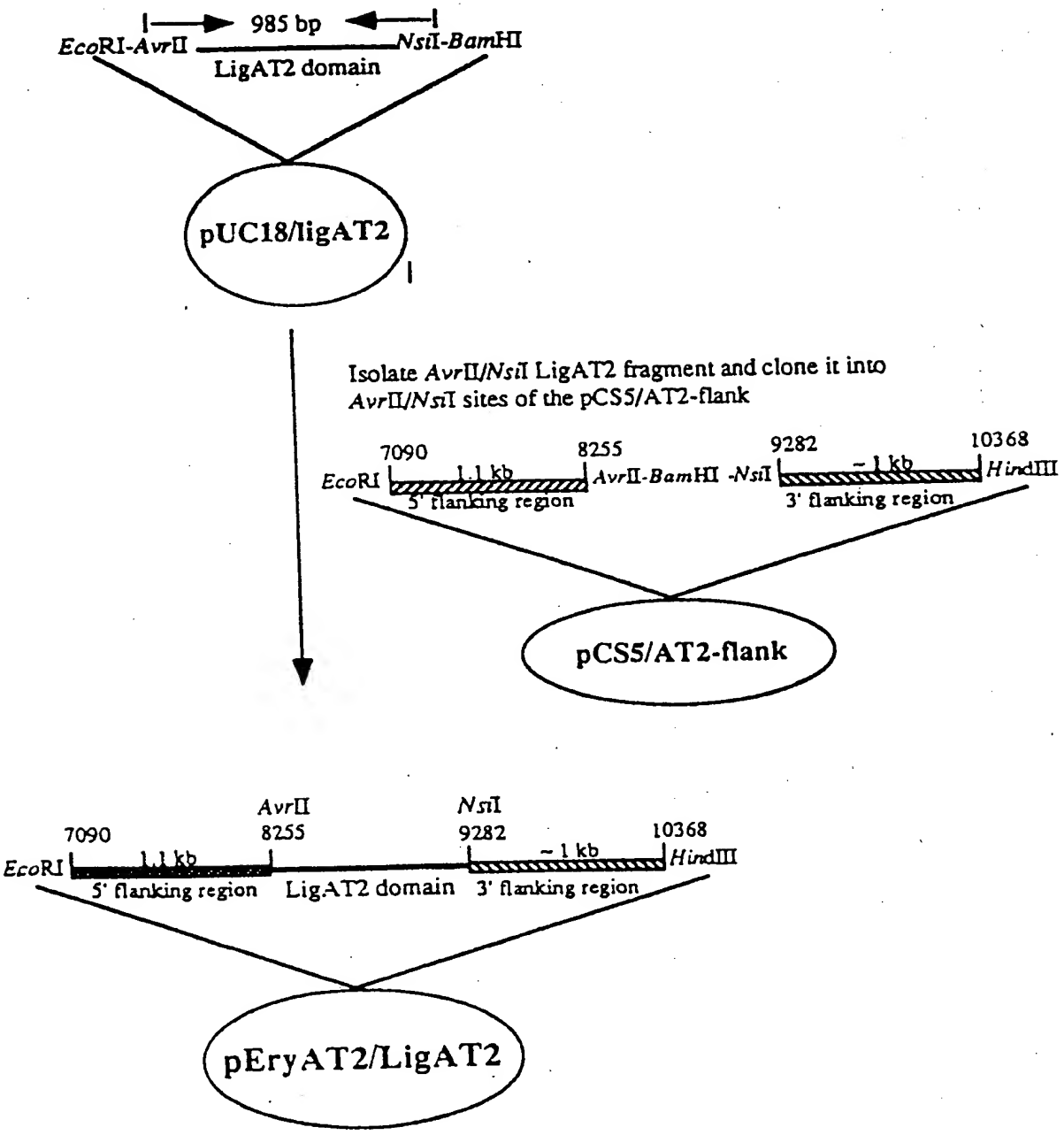


Figure 15

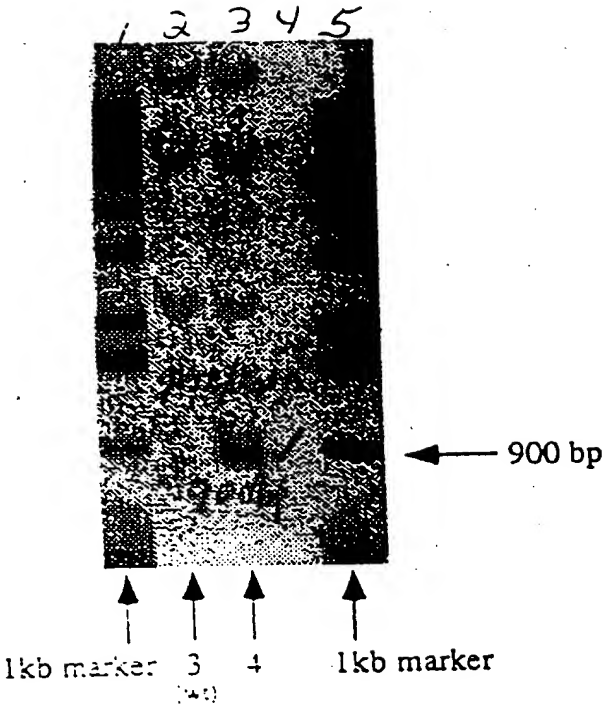


Figure 16

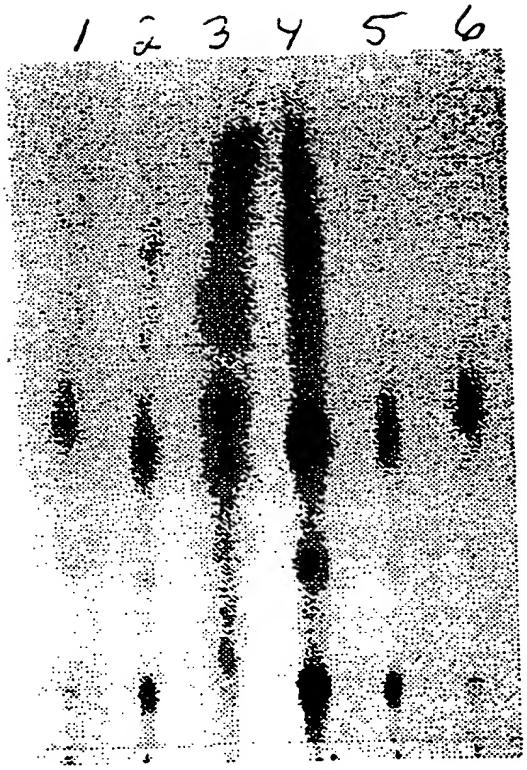


Figure 17

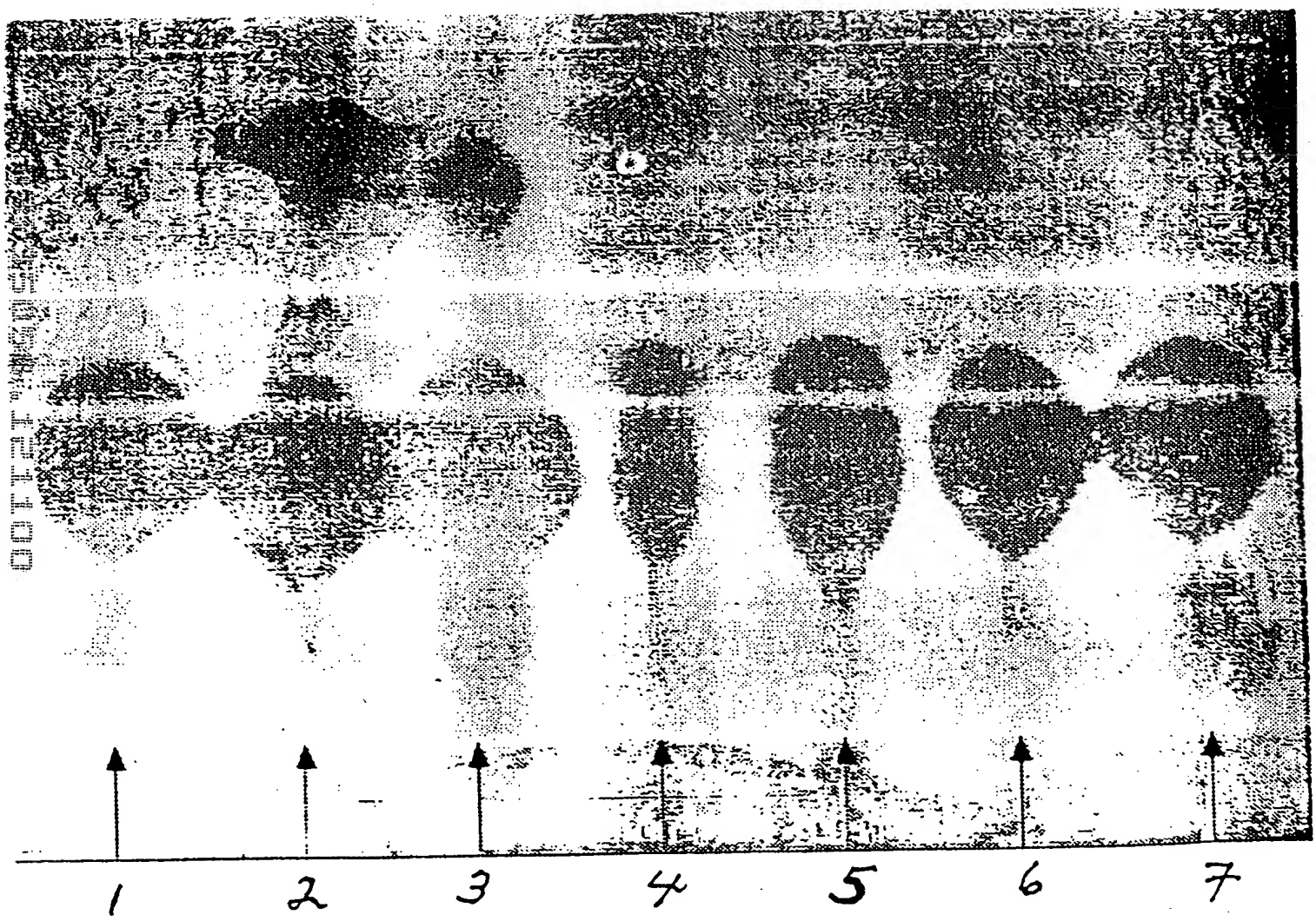


Figure 18

CCTAGGACGGCAGTCCTGCTCACCGGGCAGGGTTCCCAGCGTCAGGGCATGGGGCGCGAA 60
P R T A V L L T G Q G S Q R Q G M G R E 20

CTGTACGACCGGTCACCGGTGTTCGCCGCCTCGTTCGACGCGATCTGCGCTCAACTCGAC 120
L Y D R S P V F A A S F D A I C A Q L D 40

GGGCAACTGCCTCGTCCCCTCAAGGACGTTCTCTTCGCCCCCGAGGGGTCGGAGGACGCC 180
G Q L P R P L K D V L F A P E G S E D A 60

GCGCTCATCGACCGTACGGTGTTCACACAGGCGGCTCTGTTCGCCGTGGAGACCTCCCTG 240
A L I D R T V F T Q A A L F A V E T S L 80

TTCCGGCTGTTCGAGGCCCACGGCCTCGTCCCCGACTACCTCATCGGCCACTCCATCGGC 300
F R L F E A H G L V P D Y L I G H S I G 100

GAAGTGACCGCGGCCCACCTGGCCGGGGTCCTCGATCTGGCGGACGCGTGCGTCCTGGTC 360
E V T A A H L A G V L D L A D A C V L V 120

GCCCACCGCGGCCGCCTGATGCAGTCGGCCCGGGCCGGCGGCGCGATGGCCGCGGTCCAG 420
A H R G R L M Q S A R A G G A M A A V Q 140

GCGAGCGAGGACGAGGTACGCGAGGCCCTCGCGACCTTCGACGATGCGGTTGCCGTGGCC 480
A S E D E V R E A L A T F D D A V A V A 160

GGAGTCAACGGCCCGAACGCCACCGTCGTCTCCGGCGACGAGGACGCGGTCGAGCGGCTG 540
G V N G P N A T V V S G D E D A V E R L 180

GTCGCGCGCTGGCGCGAGCAGGGCAGGCGGACGAAGCGGCTGCCGGTCAGCCACGCCTTC 600
V A R W R E Q G R R T K R L P V S H A F 200

CACTCGCCGCACATGGACGGGATCGTCGACGAGTTCGTCACCGCCGTCTCCGGGCTCACC 660
H S P H M D G I V D E F V T A V S G L T 220

TTCCGCTCCCCGACGATCCCGGTCGTCTCCAACGTCACCGGGACCCTCGCCACCGTCGAC 720
F R S P T I P V V S N V T G T L A T V D 240

CAGCTGACCTCGCCCGCGTACTGGGCACGCCACATCCGCGAGGCCGTGCGCTTCGCCGAC 780
Q L T S P A Y W A R H I R E A V R F A D 260

GGGGTGCGGTACCTGGAGGGCGAGGGCGTCACCGAATGGCTGGAGCTCGGGCCCGACGGC 840
G V R Y L E G E G V T E W L E L G P D G 280

GTTCTCGTCGCCCTGGTCGAGGACTGCCTGGCGAAGGAGGCGGGATCGCTCGCGTCCGCC 900
V L V A L V E D C L A K E A G S L A S A 300

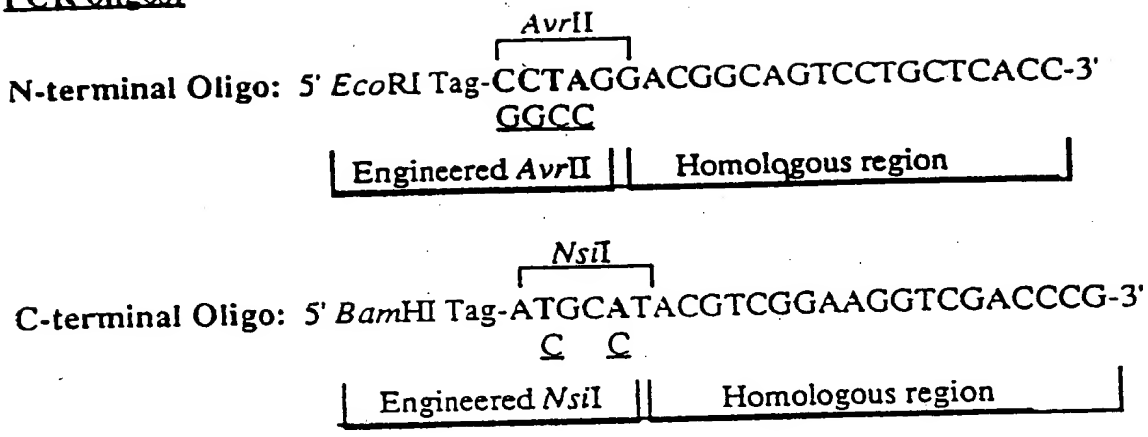
CTGCGCAAGGGGGCGAGCGAGCCCCACACCGTGGGCGCGGCCATGGCCCGCGCGGTGCTG 960
L R K G A S E P H T V G A A M A R A V L 320

CGCGGATCCGGCCCCGACTGGGCGGCGGTGTTCCCCGGCGCACGGCGGGTCGACCTTCCG 1020
R G S G P D W A A V F P G A R R V D L P 340

ACGTATGCAT 1030
T Y A 343

Figure 19

PCR oligos:



PCR cloning:

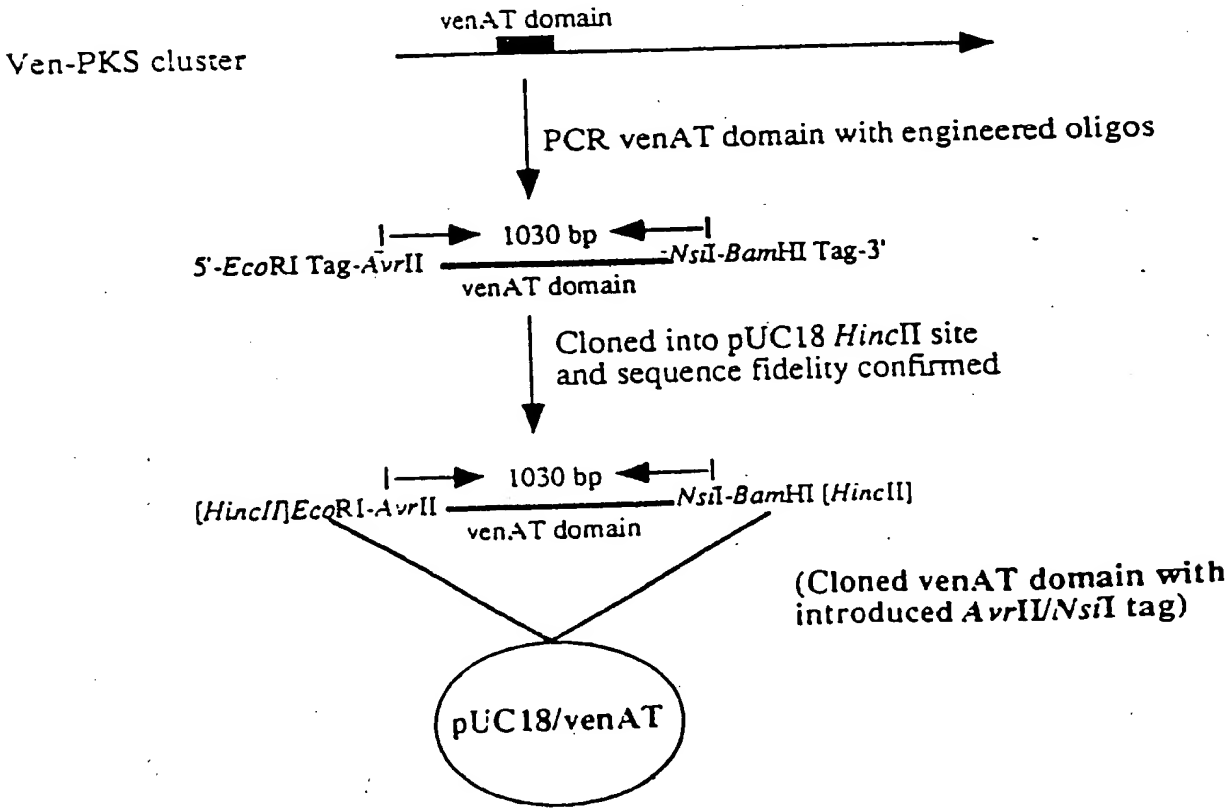


Figure 20

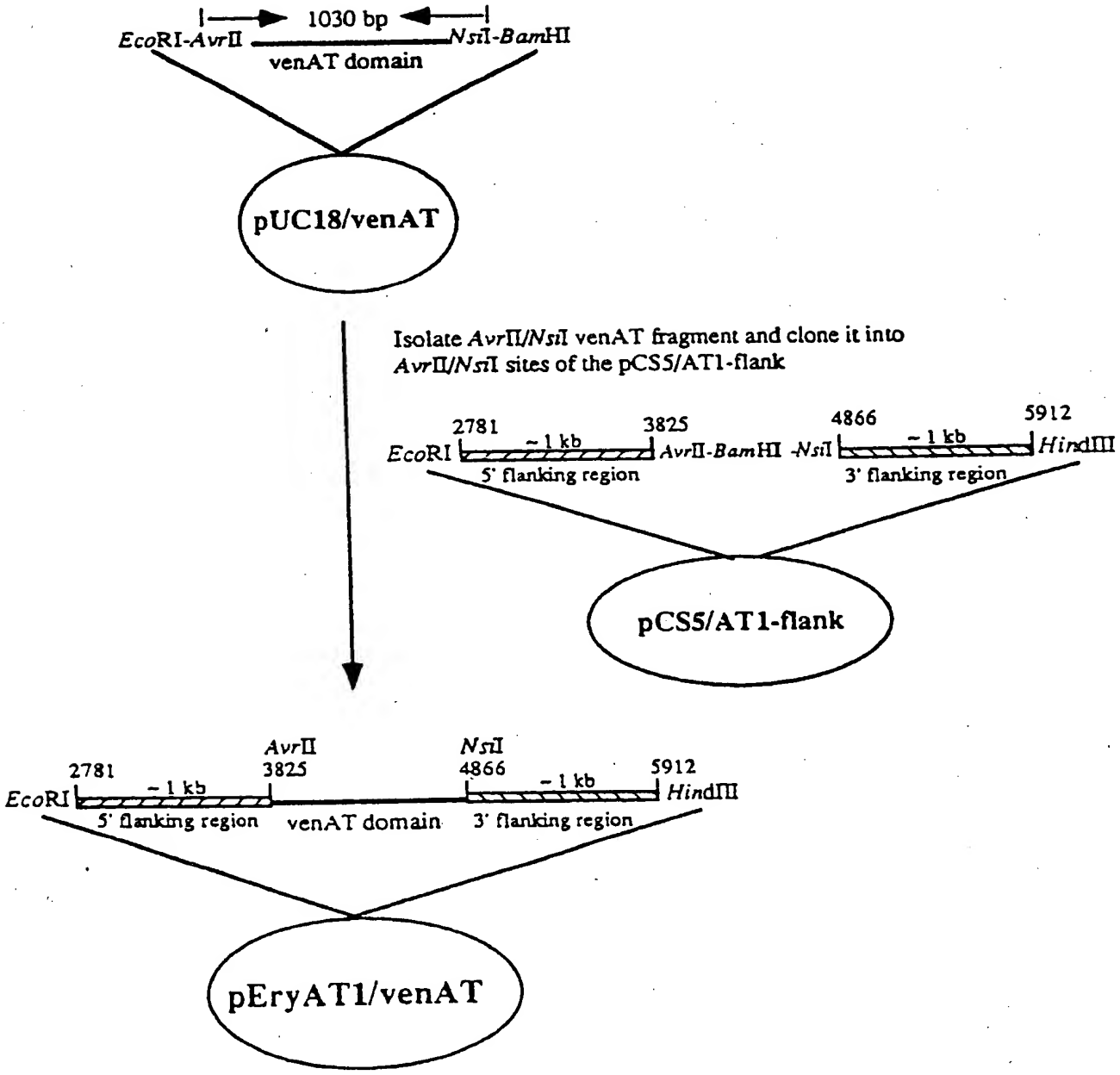

1030 bp
EcoRI-AvrII
NsiI-BamHI
venAT domain
pUC18/venAT
Isolate AvrII/NsiI venAT fragment and clone it into AvrII/NsiI sites of the pCS5/AT1-flank
2781
~ 1 kb
3825
EcoRI
AvrII-BamHI
5' flanking region
4866
~ 1 kb
5912
NsiI
HindIII
3' flanking region
pCS5/AT1-flank
AvrII
3825
NsiI
4866
2781
~ 1 kb
5912
EcoRI
~ 1 kb
HindIII
5' flanking region
venAT domain
3' flanking region
pEryAT1/venAT

Figure 21

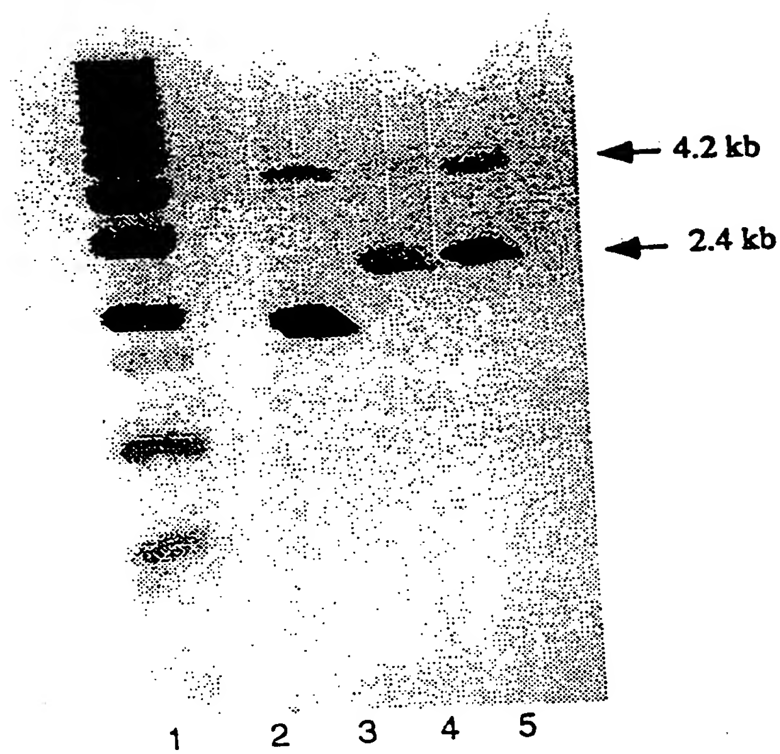


Figure 22

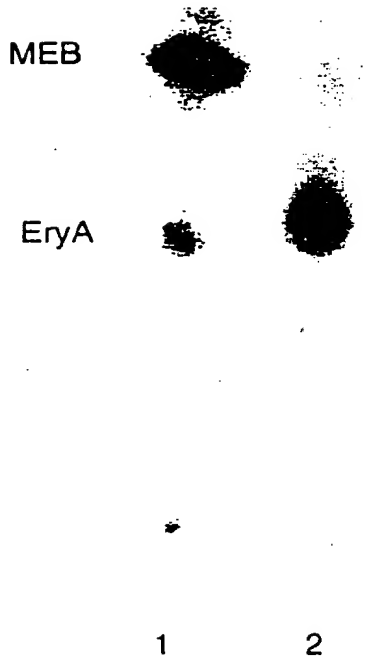
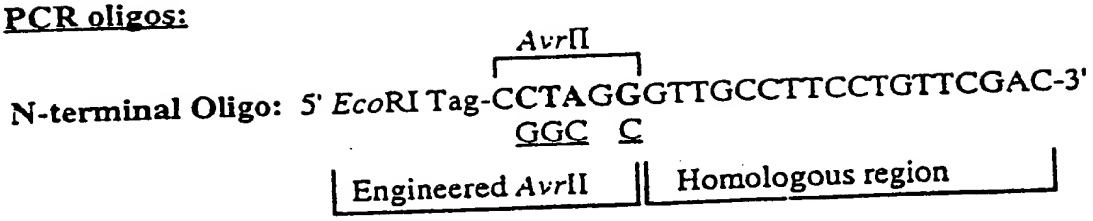
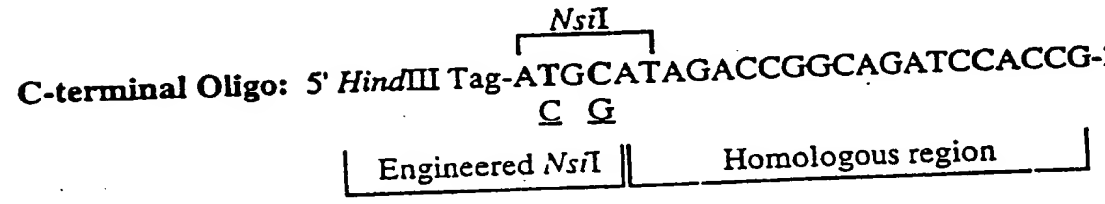


Figure 23

PCR oligos:





PCR cloning:

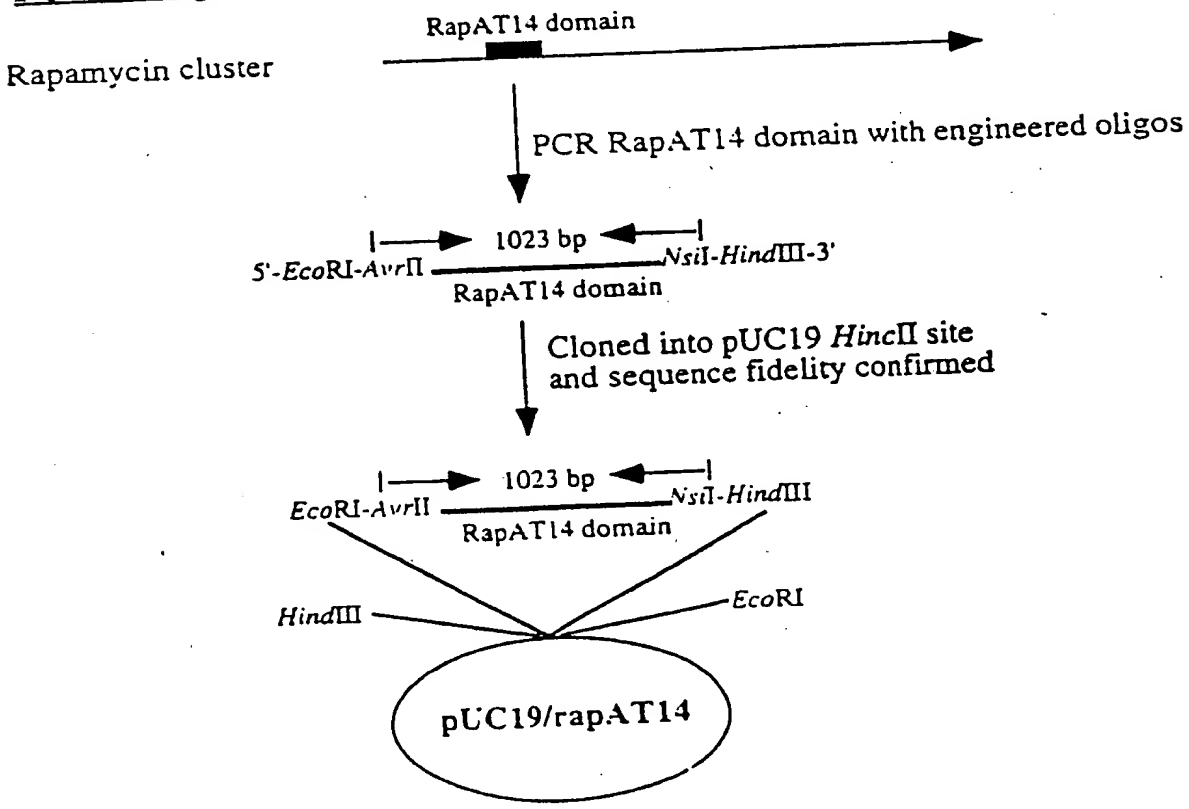


Figure 24

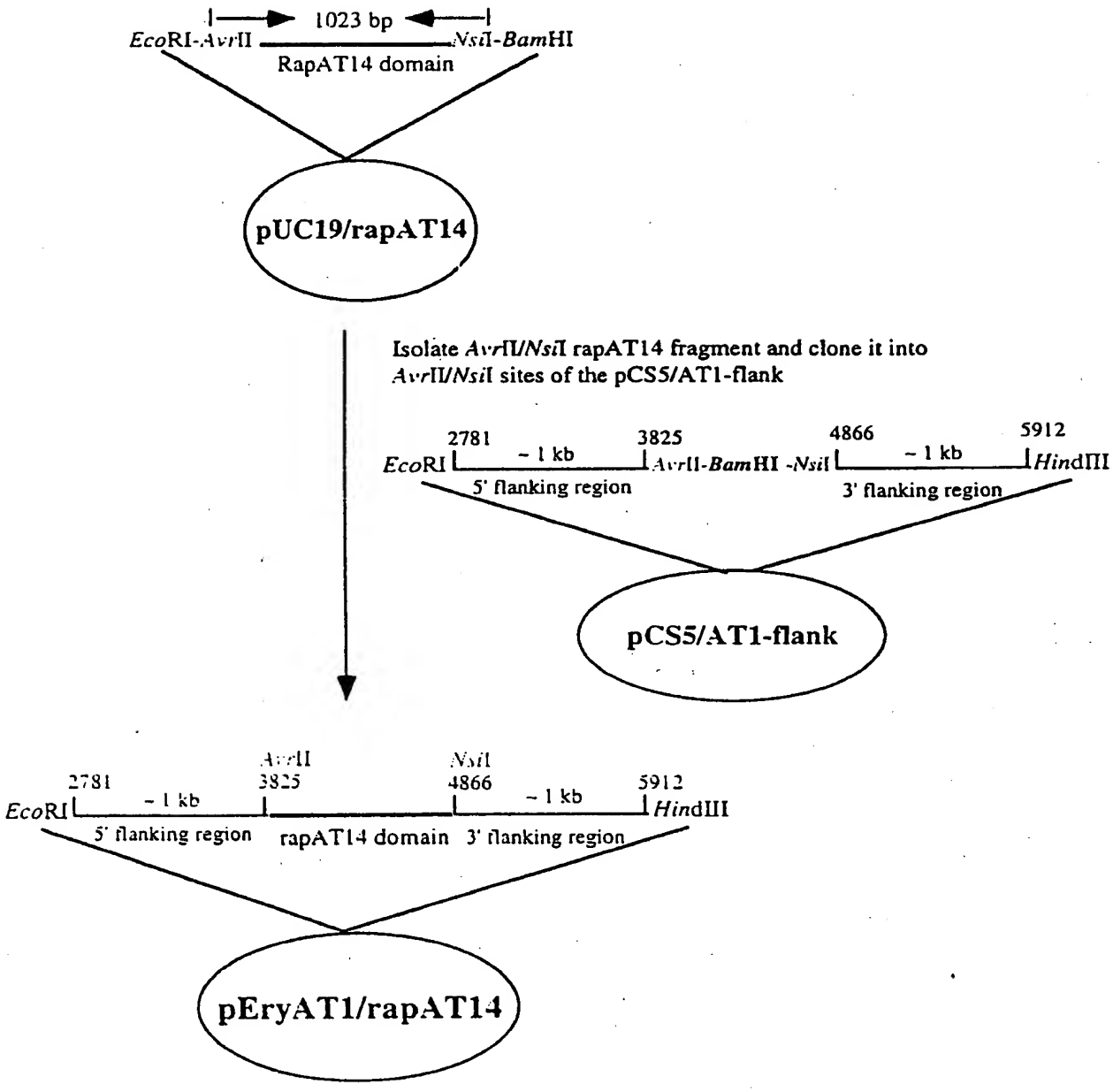

1023 bp
EcoRI-AvrII
NsiI-BamHI
RapAT14 domain
pUC19/rapAT14
Isolate AvrII/NsiI rapAT14 fragment and clone it into AvrII/NsiI sites of the pCS5/AT1-flank
2781
~ 1 kb
3825
EcoRI
AvrII-BamHI
NsiI
4866
~ 1 kb
5912
HindIII
5' flanking region
3' flanking region
pCS5/AT1-flank
AvrII
NsiI
2781
3825
4866
5912
EcoRI
~ 1 kb
~ 1 kb
HindIII
5' flanking region
rapAT14 domain
3' flanking region
pEryAT1/rapAT14

Figure 25

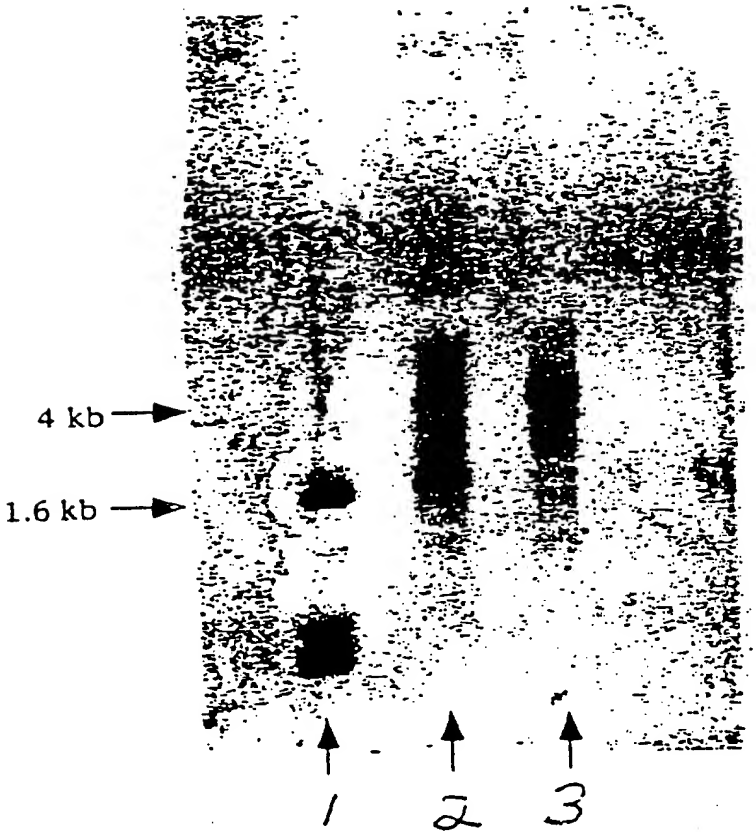
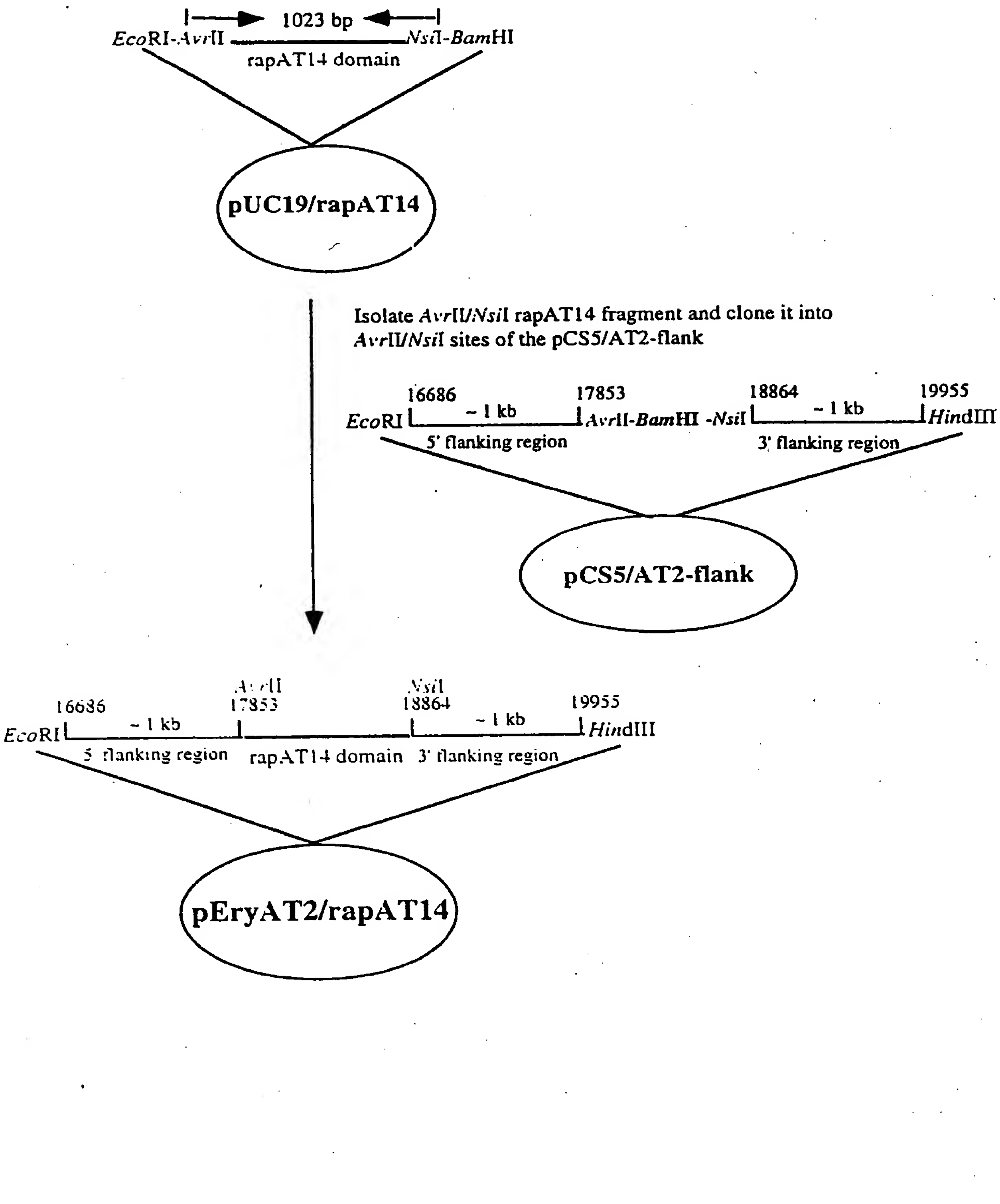


Figure 26

1 2

Figure 27



0 0 9 7 3 5 0 5 6 . 1 2 1 4 0 0

Figure 28

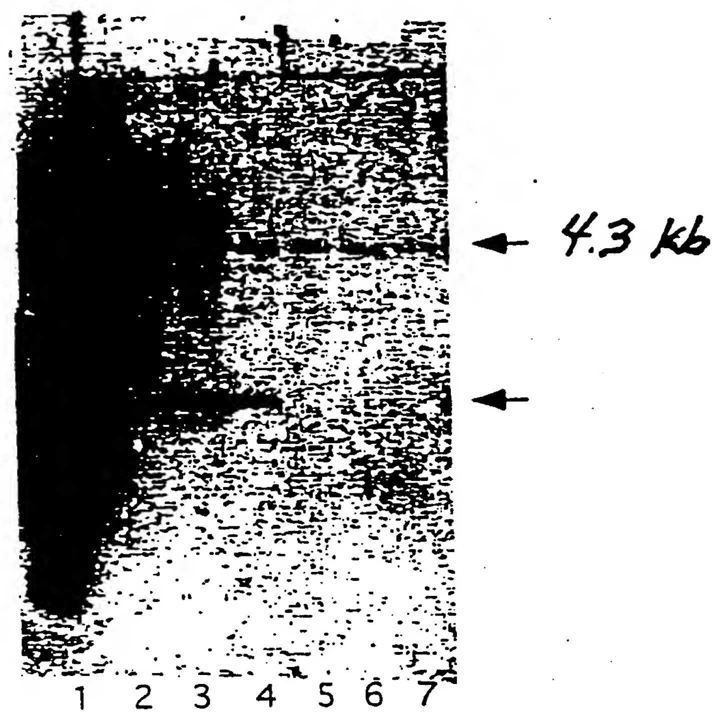


Figure 29

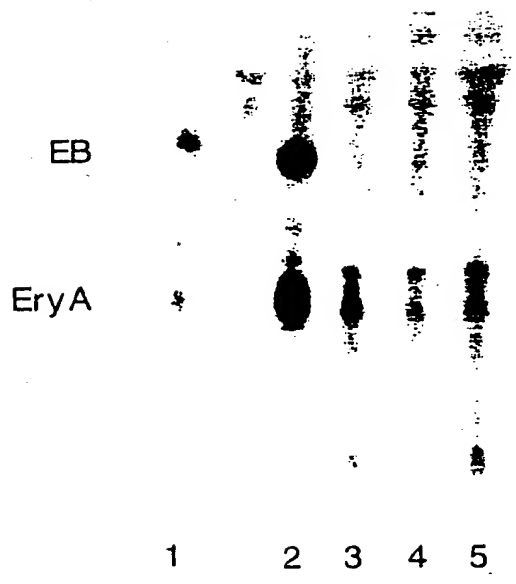


Figure 30

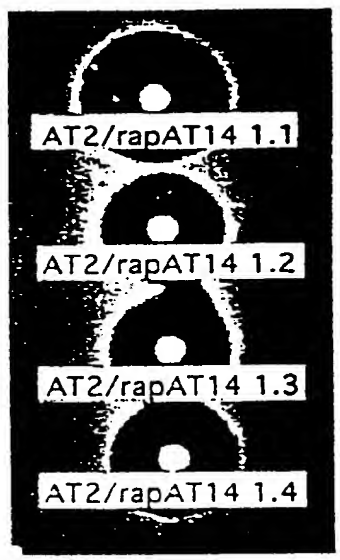


Figure 31

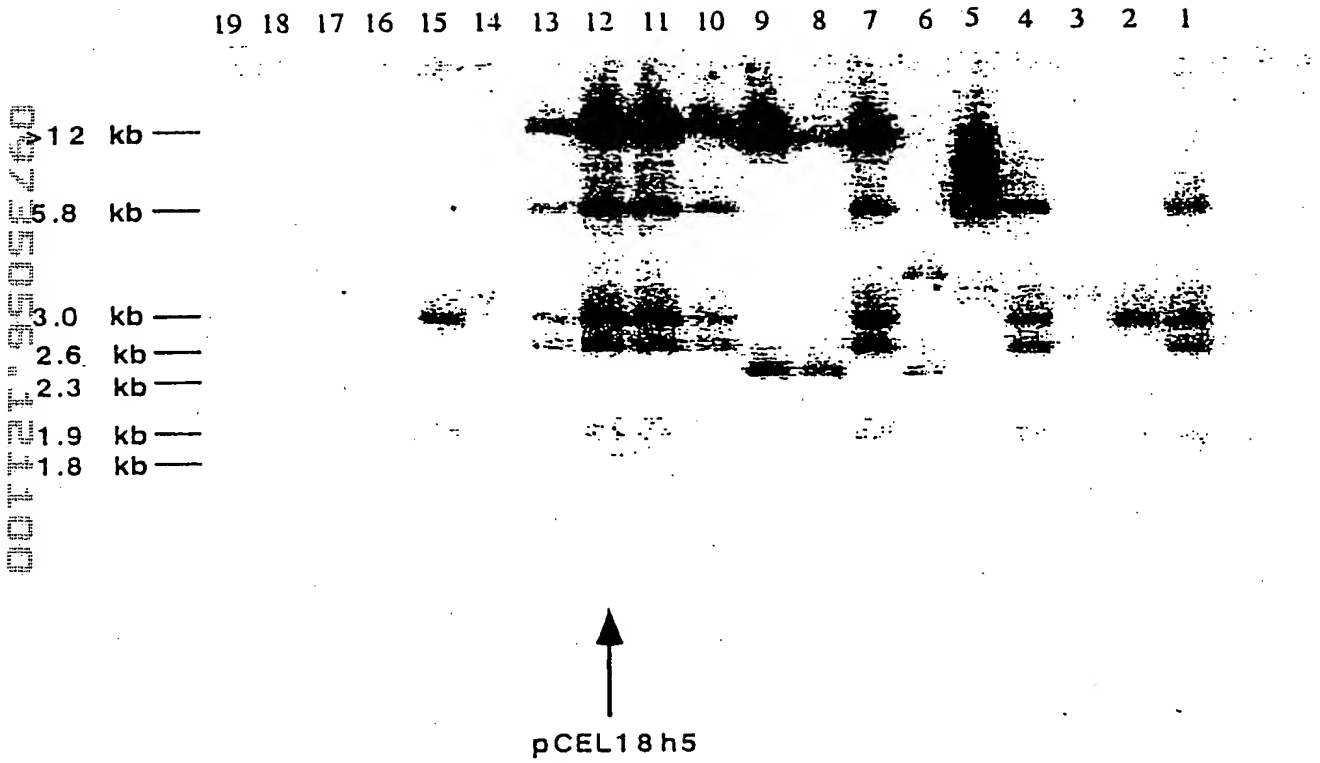

19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1
>12 kb
5.8 kb
3.0 kb
2.6 kb
2.3 kb
1.9 kb
1.8 kb
pCEL18h5

Figure 32

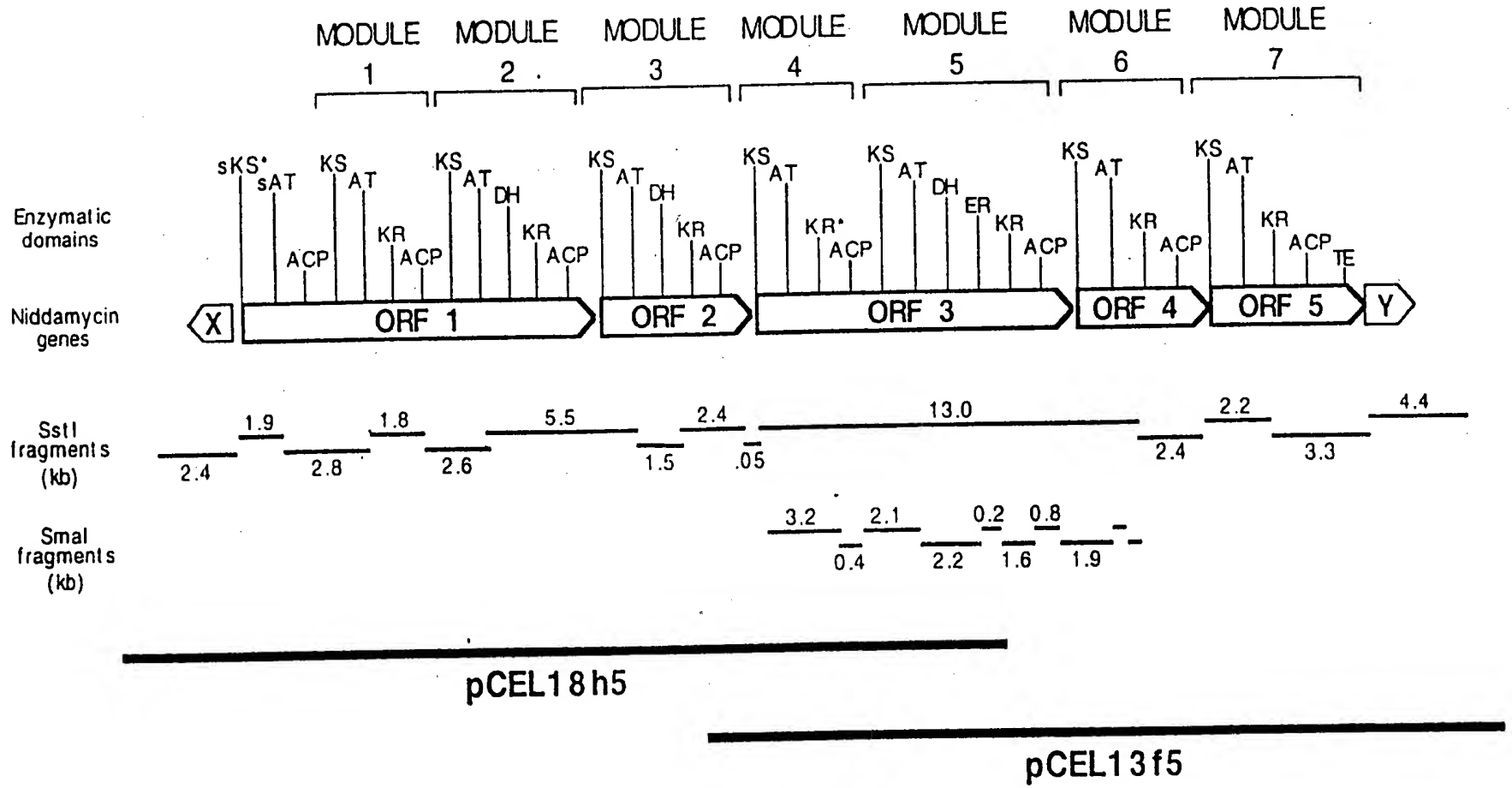


Figure 33

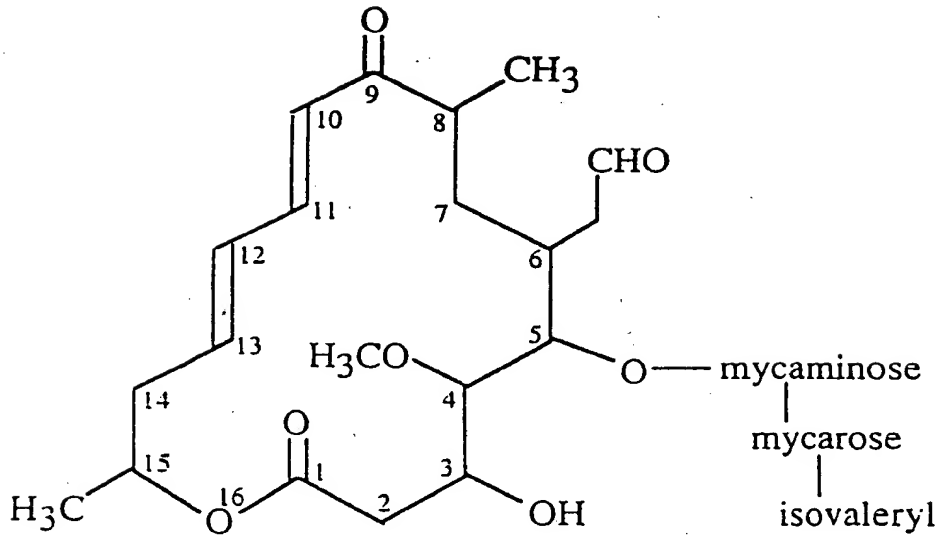

O
CH3
9
10
8
CHO
11
7
12
6
5
13
H3CO
O
mycaminose
14
4
O
mycarose
15
1
3
H3C
16
O
2
OH
isovaleryl

Figure 34

```
GCCGACCGTGTCGTGTTCGTGTTCCCCGGCCAGGGCTCGCAGTGGGCCGGAATGGCCGAG    60
A  D  R  V  V  F  V  F  P  G  Q  G  S  Q  W  A  G  M  A  E    20

GGGCTGCTGGAGCGGTCCGGCGCGTTCCGGAGTGCGGCCGACTCGTGCGACGCCGCGCTG   120
G  L  L  E  R  S  G  A  F  R  S  A  A  D  S  C  D  A  A  L    40

CGGCCGTACCTCGGCTGGTCGGTGCTGAGCGTGCTGCGCGGGGAACCGGACGCGCCCTCG   180
R  P  Y  L  G  W  S  V  L  S  V  L  R  G  E  P  D  A  P  S    60

CTCGACCGGGTCGACGTCGTGCAGCCGGTGCTGTTCACGATGATGGTCTCGCTCGCGGCG   240
L  D  R  V  D  V  V  Q  P  V  L  F  T  M  M  V  S  L  A  A    80

GTCTGGCGTGCGCTGGGGGTGGAACCGGCGGCGGTCGTCGGGCACTCGCAGGGTGAGATC   300
V  W  R  A  L  G  V  E  P  A  A  V  V  G  H  S  Q  G  E  I   100

GCCGCTGCCCATGTCGCCGGTGCGCTGTCGCTGGACGACTCGGCCCGGATCGTCGCCCTG   360
A  A  A  H  V  A  G  A  L  S  L  D  D  S  A  R  I  V  A  L   120

CGCAGTCGGGCGTGGCTCGGACTGGCGGGCAAGGGCGGCATGGTGGCGGTGCCGATGCCG   420
R  S  R  A  W  L  G  L  A  G  K  G  G  M  V  A  V  P  M  P   140

GCGGAGGAGCTGCGGCCGCGGCTGGTGACGTGGGGGGACCGTCTGGCCGTCGCCGCCGTC   480
A  E  E  L  R  P  R  L  V  T  W  G  D  R  L  A  V  A  A  V   160

AACAGCCCCGGTTCCTGCGCCGTCGCAGGCGACCCGGAGGCGCTGGCCGAACTGGTGGCG   540
N  S  P  G  S  C  A  V  A  G  D  P  E  A  L  A  E  L  V  A   180

CTGCTGACCGGTGAGGGGGTGCACGCCCGGCCGATCCCCGGCGTCGACACGGCGGGCCAC   600
L  L  T  G  E  G  V  H  A  R  P  I  P  G  V  D  T  A  G  H   200

TCGCCGCAGGTGGACGCGTTGCGGGCTCATCTGCTGGAGGTGCTGGCCCCGGTCGCCCCC   660
S  P  Q  V  D  A  L  R  A  H  L  L  E  V  L  A  P  V  A  P   220

CGACCGGCCGACATCCCGTTCTACTCGACGGTGACCGGCGGGCTGCTGGACGGCACCGAG   720
R  P  A  D  I  P  F  Y  S  T  V  T  G  G  L  L  D  G  T  E   240

CTGGACGCGACGTACTGGTACCGCAACATGCGCGAGCCCGTCGAGTTCGAGCGGGCCACA   780
L  D  A  T  Y  W  Y  R  N  M  R  E  P  V  E  F  E  R  A  T   260

CGGGCGCTGATCGCCGACGGGCACGACGTCTTCCTGGAGACGAGCCCGCATCCCATGCTG   840
R  A  L  I  A  D  G  H  D  V  F  L  E  T  S  P  H  P  M  L   280

GCCGTGGCGCTGGAGCAGACGGTCACCGACGCCGGCACCGACGCGGCGGTGCTCGGGACC   900
A  V  A  L  E  Q  T  V  T  D  A  G  T  D  A  A  V  L  G  T   300

CTGCGCCGCCGCCACGGCGGTCCTCGCGCGCTGGCCCTGGCCGTCTGCCGCGCCTTCGCG   960
L  R  R  R  H  G  G  P  R  A  L  A  L  A  V  C  R  A  F  A   320

CACGGCGTGGAGGTGGACCCCGAGGCGGTCTTCGGTCCGGGCGCACGGCCCGTGGAGTTG  1020
H  G  V  E  V  D  P  E  A  V  F  G  P  G  A  R  P  V  E  L   340

CCCACCTATCCG  1032
P  T  Y  P   344
```

Figure 35

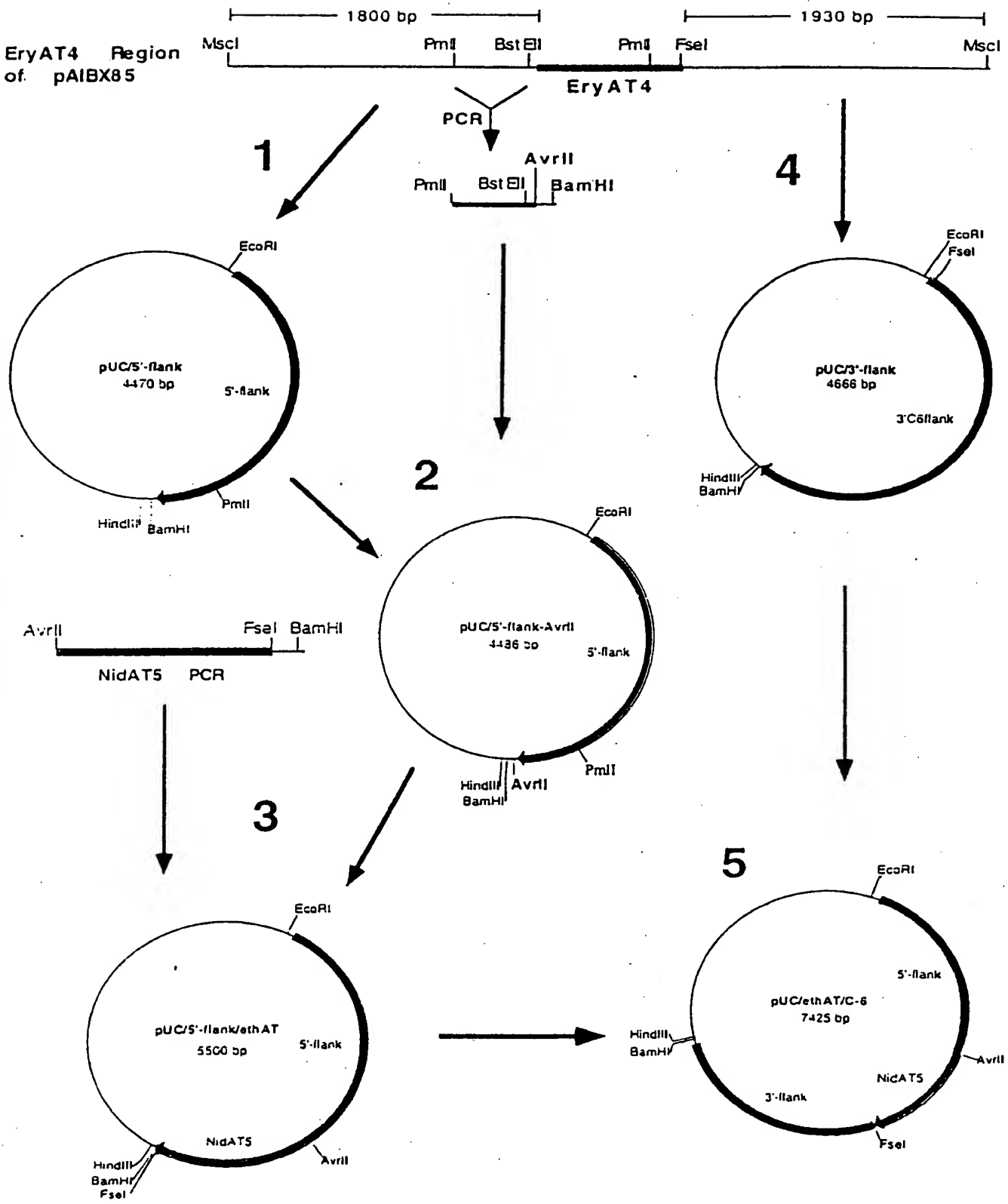
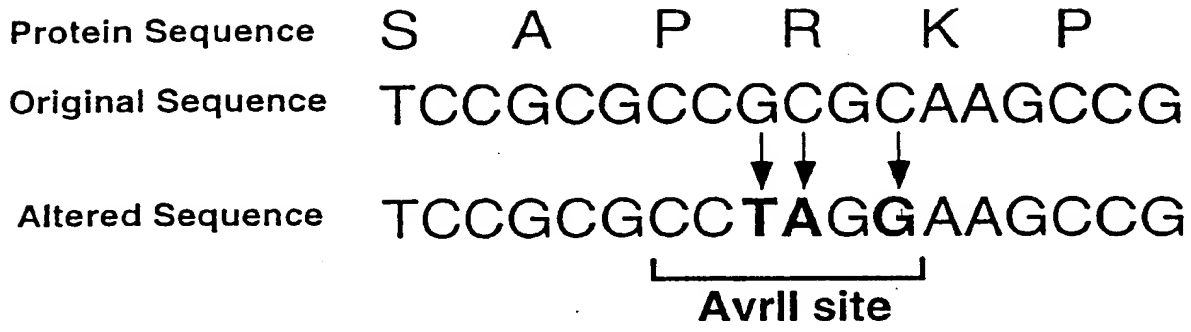
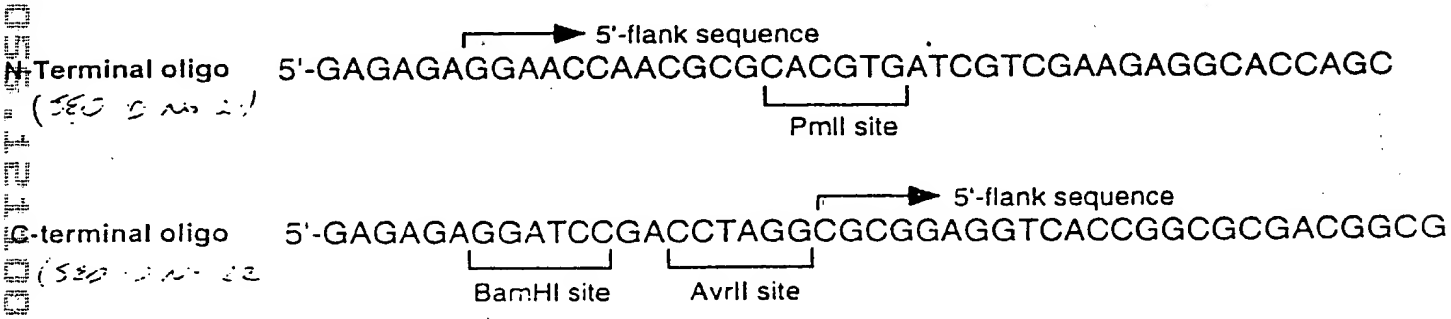

1800 bp
1930 bp
EryAT4 Region of pAIBX85
MscI
PmlI
BstEII
PmlI
FseI
MscI
EryAT4
PCR
AvrII
PmlI
BstEII
BamHI
1
2
3
4
5
EcoRI
pUC/5'-flank
4470 bp
5'-flank
PmlI
HindIII
BamHI
pUC/3'-flank
4666 bp
3'C6flank
FseI
HindIII
BamHI
pUC/5'-flank-AvrII
4486 bp
AvrII
FseI
BamHI
NidAT5 PCR
pUC/5'-flank/ethAT
5500 bp
NidAT5
pUC/ethAT/C-6
7425 bp
3'-flank

Figure 36



PCR Oligos for 5'-flank AvrII site



PCR oligos for NidAT5 fragment

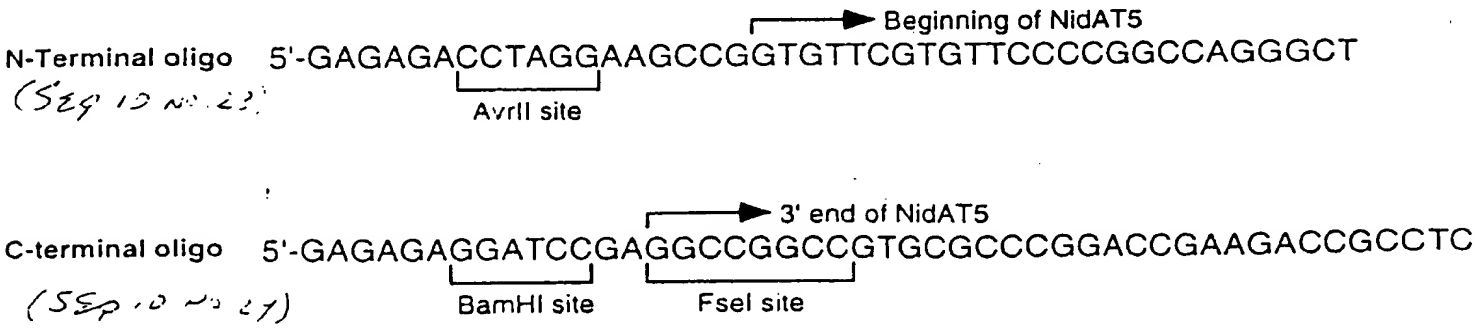


Figure 37

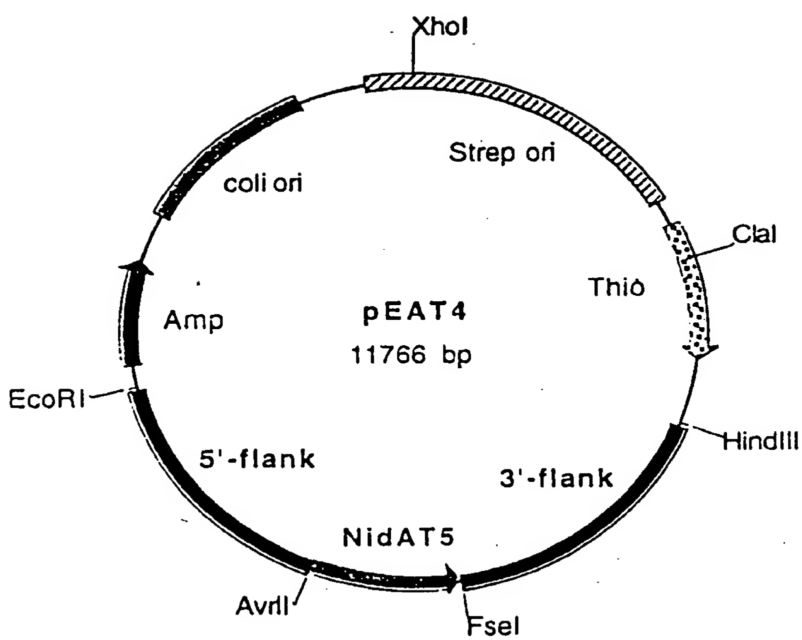


Figure 38

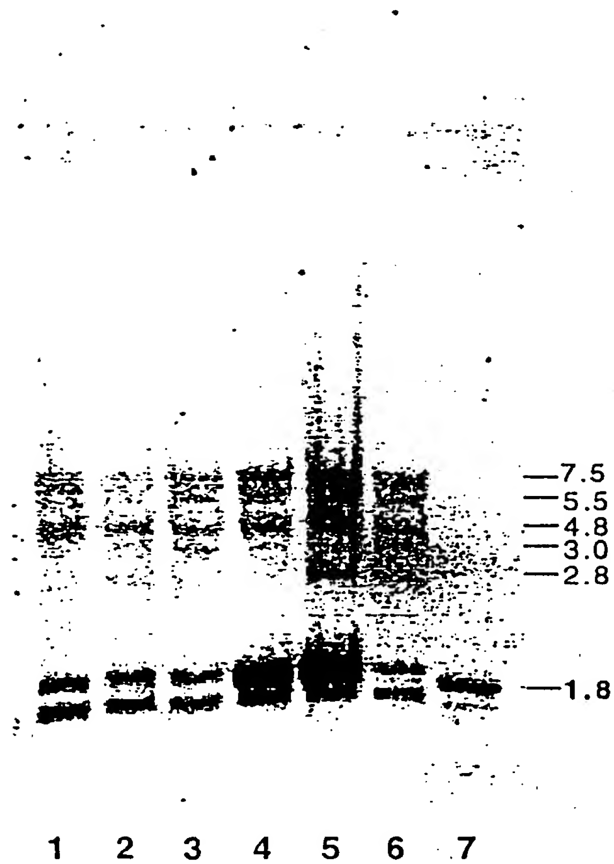
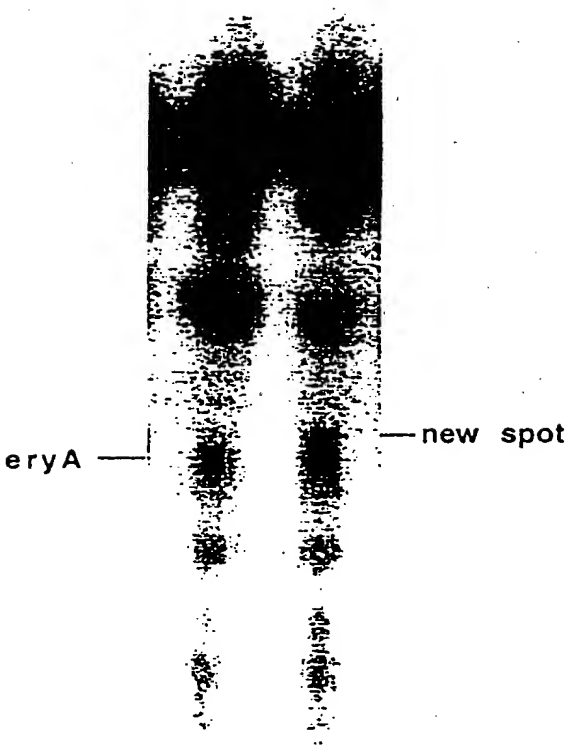


Figure 39



A) SCM only

B) SCM + 50mM butyric acid

A B

Figure 40

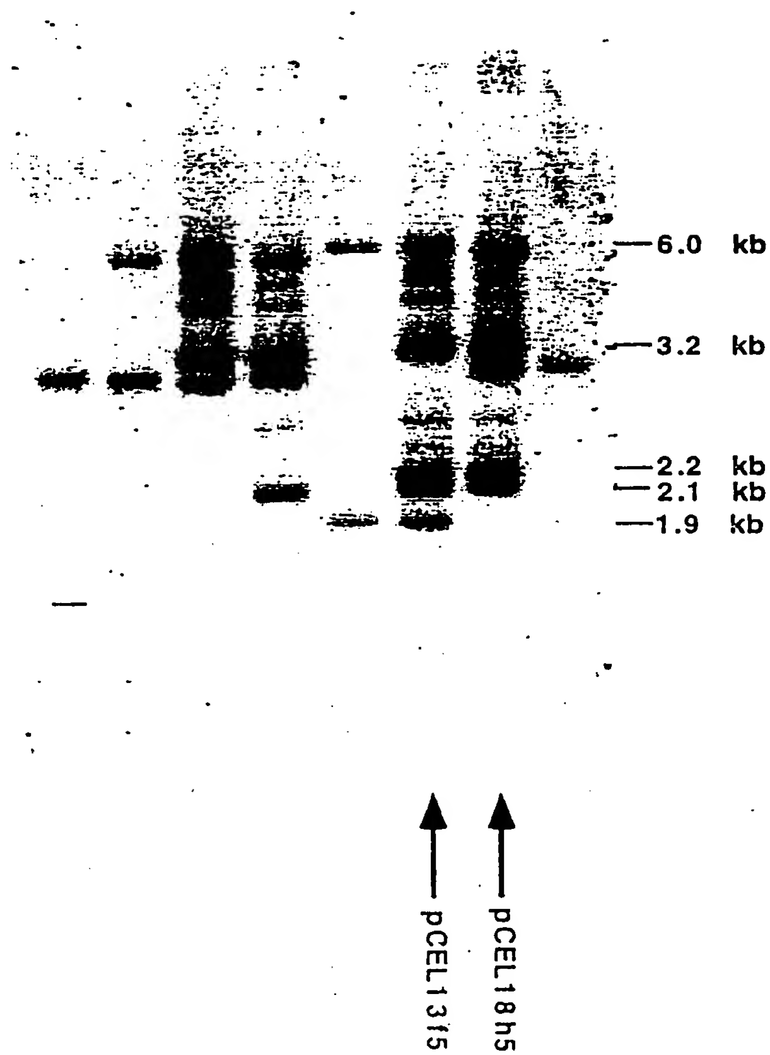


Figure 41

```
CGCGCGCCTGCCTTCGTCTTTCCCGGGCAGGGCGCCCAGTGGGCCGGACTGGGAGCGCGG    60
R  A  P  A  F  V  F  P  G  Q  G  A  Q  W  A  G  L  G  A  R   20

CTCCTCGCGGACTCCCCCGTCTTCCGCGCCAGGGCCGAGGCATGCGCGCGGGCGCTGGAG   120
L  L  A  D  S  P  V  F  R  A  R  A  E  A  C  A  R  A  L  E   40

CCTCACCTCGACTGGTCGGTCCTCGACGTGCTGGCCGGCGCCCCGGGCACCCCTCCCATC   180
P  H  L  D  W  S  V  L  D  V  L  A  G  A  P  G  T  P  P  I   60

GACCGGGCCGACGTGGTGCAGCCGGTGCTGTTCACCACGATGGTCTCGCTGGCCGCCCTC   240
D  R  A  D  V  V  Q  P  V  L  F  T  T  M  V  S  L  A  A  L   80

TGGGAGGCCCACGGGGTGCGGCCGGCCGCGGTCGTGGGCCACTCCCAGGGCGAGGTGGCC   300
W  E  A  H  G  V  R  P  A  A  V  V  G  H  S  Q  G  E  V  A  100

GCGGCCTGCGTGGCCGGTGCCCTGTCGCTGGACGACGCTGCCCTGGTGATCGCCGGACGC   360
A  A  C  V  A  G  A  L  S  L  D  D  A  A  L  V  I  A  G  R  120

AGCAGGCTGTGGGGGCGGCTGGCCGGGAACGGCGGGATGCTCGCGGTGATGGCTCCGGCC   420
S  R  L  W  G  R  L  A  G  N  G  G  M  L  A  V  M  A  P  A  140

GAGCGGATCCGTGAGCTGCTCGAACCATGGCGGCAGCGGATTTCGGTGGCGGCGGTCAAT   480
E  R  I  R  E  L  L  E  P  W  R  Q  R  I  S  V  A  A  V  N  160

GGCCCCGCCTCGGTCACCGTCTCCGGTGACGCGCTCGCGCTGGAGGAGTTCGGCGCGCGG   540
G  P  A  S  V  T  V  S  G  D  A  L  A  L  E  E  F  G  A  R  180

CTCTCCGCCGAGGGGGTGCTGCGCTGGCCGCTGCCGGGCGTCGACTTCGCCGGCCACTCG   600
L  S  A  E  G  V  L  R  W  P  L  P  G  V  D  F  A  G  H  S  200

CCGCAGGTGGAGGAGTTCCGCGCTGAGCTCCTGGACCTGCTCTCCGGCGTACGGCCGGCT   660
P  Q  V  E  E  F  R  A  E  L  L  D  L  L  S  G  V  R  P  A  220

CCTTCGCGGATACCTTTCTTCTCCACCGTGACGGCGGGTCCTTGCGGCGGCGACCAGCTG   720
P  S  R  I  P  F  F  S  T  V  T  A  G  P  C  G  G  D  Q  L  240

GACGGGGCGTACTGGTACCGCAACACGCGCGAACCCGTGGAGTTCGACGCCACGGTCCGG   780
D  G  A  Y  W  Y  R  N  T  R  E  P  V  E  F  D  A  T  V  R  260

GCGCTGCTGCGTGCGGGCCATCACACGTTCATCGAGGTCGGTCCGCATCCGCTGCTCAAC   840
A  L  L  R  A  G  H  H  T  F  I  E  V  G  P  H  P  L  L  N  280

GCCGCGATCGACGAGATCGCAGCGGACGAGGGGGTAGCGGCCACGGCCCTGCATACGCTC   900
A  A  I  D  E  I  A  A  D  E  G  V  A  A  T  A  L  H  T  L  300

CAGCGGGGCGCTGGCGGCCTTGACCGCGTGCGCAACGCGGTGGGCGCCGCTTTCGCGCAC   960
Q  R  G  A  G  G  L  D  R  V  R  N  A  V  G  A  A  F  A  H  320

GGTGTCCGGGTCGACTGGAACGCCCTGTTCGAGGGCACCGGTGCGCGCAGGGTGCCGCTT  1020
G  V  R  V  D  W  N  A  L  F  E  G  T  G  A  R  R  V  P  L  340

CCCTCGTACGCCTTC  1035
P  S  Y  A  F  345
```

Figure 42

PCR oligos:

*Avr*II

N-terminal Oligo: 5' *Eco*RI Tag-CCTAGGGTCGCCTTCGTCTTTCCCGGGCAGG-3'
GCGC CCT

Engineered *Avr*II and Val codon | Homologous region

*Nsi*I

C-terminal Oligo: 5' *Bgl*II Tag-ATGCATACGAGGGAAGCGGCACCCTGC-3'
G G

Engineered *Nsi*I | Homologous region

PCR cloning:

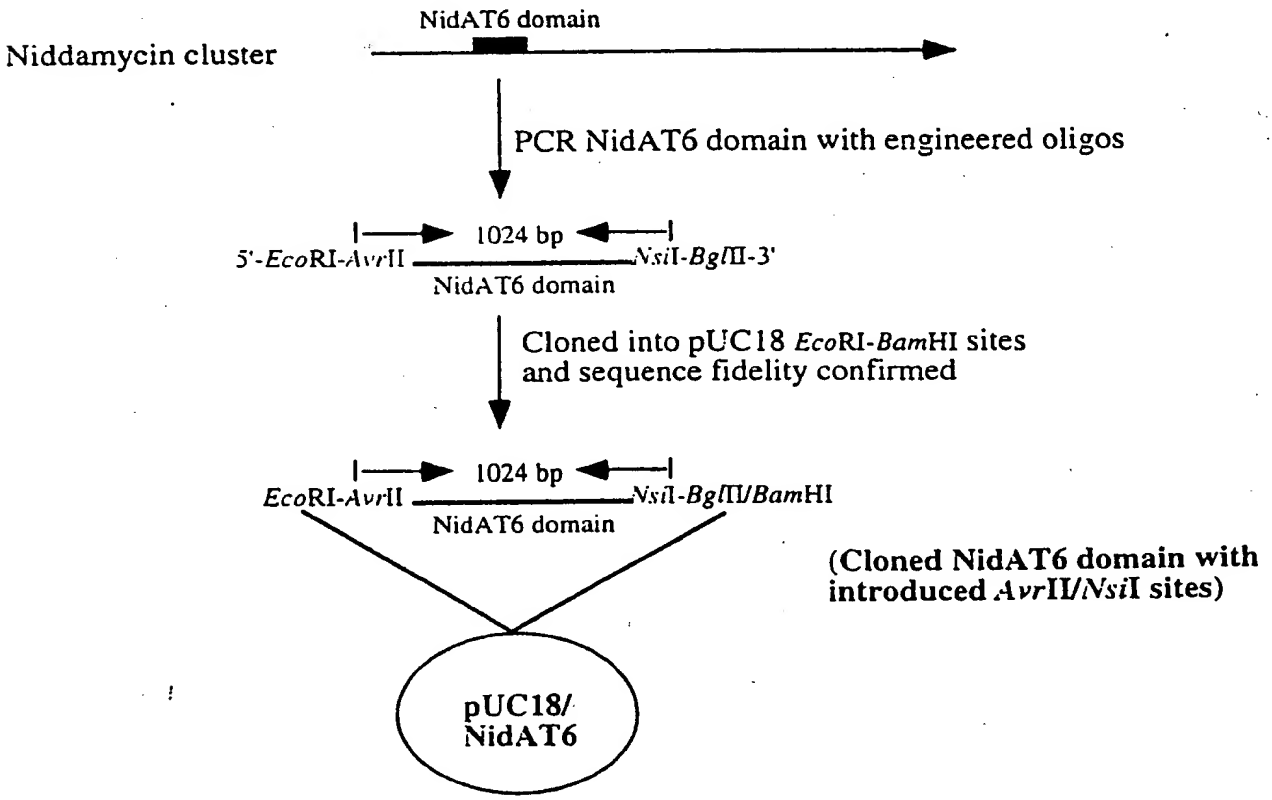
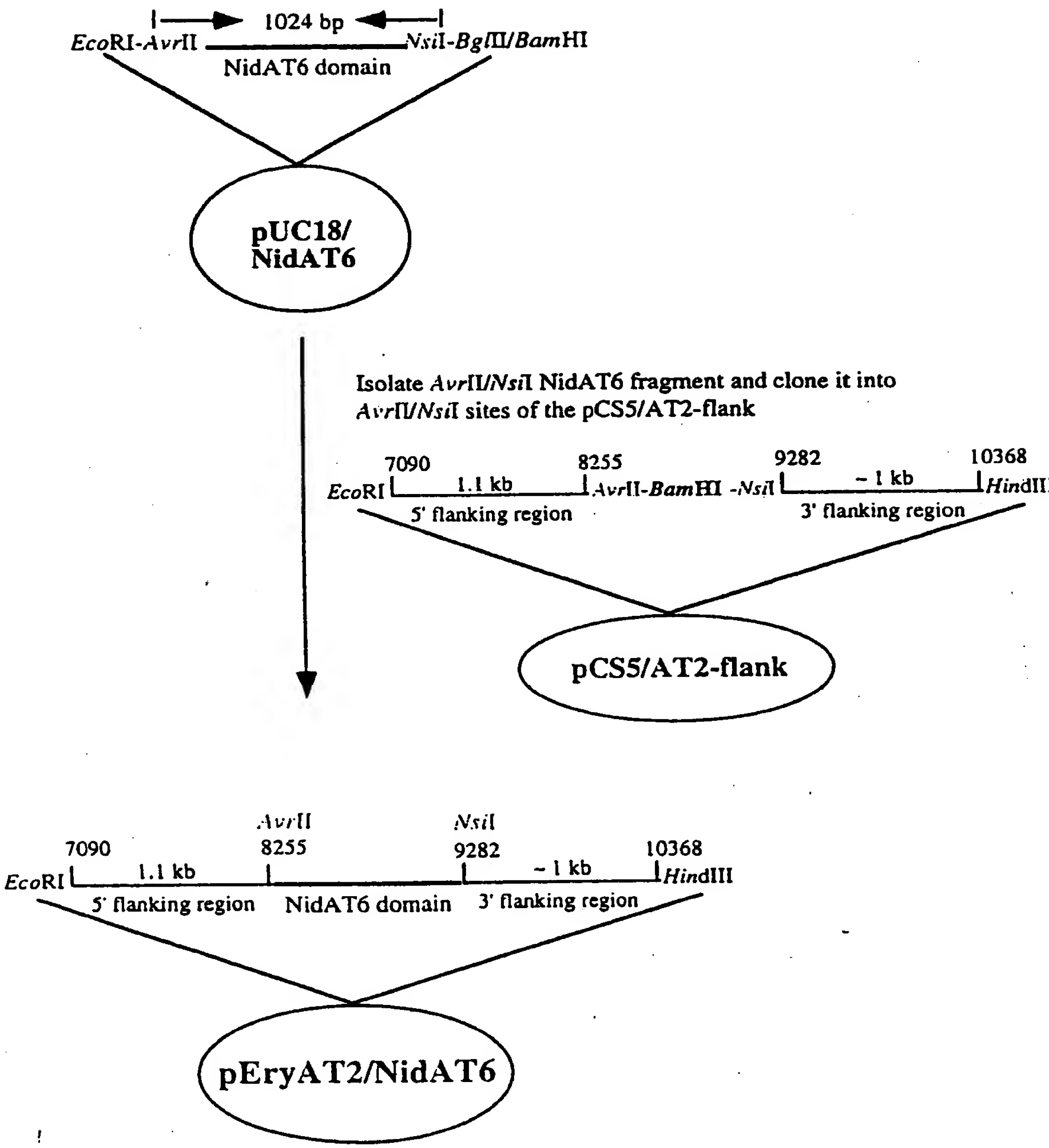


Figure 43


1024 bp
EcoRI-AvrII
NsiI-BglII/BamHI
NidAT6 domain
pUC18/
NidAT6
Isolate AvrII/NsiI NidAT6 fragment and clone it into
AvrII/NsiI sites of the pCS5/AT2-flank
7090
8255
9282
10368
EcoRI
1.1 kb
AvrII-BamHI -NsiI
~ 1 kb
HindIII
5' flanking region
3' flanking region
pCS5/AT2-flank
AvrII
NsiI
7090
8255
9282
10368
EcoRI
1.1 kb
~ 1 kb
HindIII
5' flanking region
NidAT6 domain
3' flanking region
pEryAT2/NidAT6